

Result No.	Score	Query Match	Length	DB ID	Description
1	4063	100.0	801	4	US-10-600-070-2
2	4051	99.7	801	4	US-10-600-070-127
3	4051	99.7	801	4	US-10-600-070-129
4	4051	99.7	801	4	US-10-600-070-131
5	4051	99.7	801	5	US-10-739-930-5771
6	2226	72.0	578	4	US-10-600-070-123
7	1775.5	43.7	760	4	US-10-600-070-125
8	1646	40.5	324	4	US-10-600-070-206
9	1332	32.8	525	4	US-10-600-070-122
10	1134	27.9	344	4	US-10-424-599-271849
11	973	23.9	364	4	US-10-425-115-266516
12	972	23.9	480	4	US-10-437-963-172416
13	856	21.1	416	4	US-10-425-115-242115
14	522.5	12.9	768	4	US-10-600-070-167
15	499	12.3	204	4	US-10-424-599-177901
16	498.5	12.3	789	4	US-10-600-070-194
17	497	12.2	798	4	US-10-600-070-164
18	497	12.2	798	4	US-10-600-070-165
19	482	11.9	709	4	US-10-437-963-172415
20	474.5	11.7	1157	4	US-10-437-963-155799
21	442	10.9	631	4	US-10-600-070-5
22	442	10.9	631	4	US-10-600-070-162
23	435.5	10.7	191	4	US-10-767-701-35633
24	434.5	10.7	624	4	US-10-600-070-116
25	431	10.6	819	4	US-10-600-070-171
26	431	10.6	819	4	US-10-600-070-173
27	429	10.6	714	4	US-10-600-070-169

Qy	361 FIGRKPHLQDADQFQOLQQAKVMAEIPAMLYDTRNNWEIDFGLERGLCAALLIGRVE 420	Db	181 GETEIVLRVGEALLKERLPKSFQDVVLMALAFDVSRDAMALDPDFITGYBFVVEAL 240
Db	361 FIGRKPHLQDADQFQOLQQAKVMAEIPAMLYDTRNNWEIDFGLERGLCAALLIGRVE 420	Qy	241 KLIQEEGASSLAPPDLRAQIDETTEITTPRYVELLGPIGDDYAAKRNLNGLSGVRNLLWS 300
Qy	421 CRMWGLDSESDQRNPNAIVEFYLENSNRDNDLPGIICKLLETTMLAGVVFPRFRDTKDK 480	Db	241 KLIQEEGASSLAPPDLRAQIDETTEITTPRYVELLGPIGDDYAAKRNLNGLSGVRNLLWS 300
Db	421 CRMWGLDSESDQRNPNAIVEFYLENSNRDNDLPGIICKLLETTMLAGVVFPRFRDTKDK 480	Qy	301 VGGGGASALVGGLTREKFNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALVAQA 360
Qy	481 KFKLGDXYYDDPMVLSYLERYVEVQGSPLAAATTMARGAEHYKASANQALQYKUPPSYTD 540	Db	301 VGGGGASALVGGLTREKFNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALVAQA 360
Db	481 KFKLGDXYYDDPMVLSYLERYVEVQGSPLAAATTMARGAEHYKASANQALQYKUPPSYTD 540	Qy	361 FIGRKPHLQDADQFQOLQQAKVMAEIPAMLYDTRNNWEIDFGLERGLCAALLIGKVDE 420
Qy	541 RNSAEPKDVOQETVSVDPGNNVGRDGEPPGVFAEAVRPSENFTNDYAIRAGVSESSVD 600	Db	361 FIGRKPHLQDADQFQOLQQAKVMAEIPAMLYDTRNNWEIDFGLERGLCAALLIGKVDE 420
Db	541 RNSAEPKDVOQETVSVDPGNNVGRDGEPPGVFAEAVRPSENFTNDYAIRAGVSESSVD 600	Qy	421 CRMWGLDSESDQRNPALIVEFYLENSNRDNDLPGIICKLLETTMLAGVVFPRFRDTKDK 480
Qy	601 ETIVEMSYADMILKEASVTKLAAAGVAGIQLISLFSQYKFLKSSESSFORKDMVSSMESDVATI 660	Db	421 CRMWGLDSESDQRNPALIVEFYLENSNRDNDLPGIICKLLETTMLAGVVFPRFRDTKDK 480
Db	601 ETIVEMSYADMILKEASVTKLAAAGVAGIQLISLFSQYKFLKSSESSFORKDMVSSMESDVATI 660	Qy	481 KFKLGDXYYDDPMVLSYLERYVEVQGSPLAAATTMARGAEHYKASANQALQYKUPPSYTD 540
Qy	661 GSTRADDSSEALPRMDARTAENITYSKWQKIKSLAFLGPDHRIEMLPEVLDGRMLKIWTDRRA 720	Db	481 KFKLGDXYYDDPMVLSYLERYVEVQGSPLAAATTMARGAEHYKASANQALQYKUPPSYTD 540
Db	661 GSTRADDSSEALPRMDARTAENITYSKWQKIKSLAFLGPDHRIEMLPEVLDGRMLKIWTDRRA 720	Qy	541 RNSAEKPDKOQETVFSVPDVGNNYGRDGEPPGVFAEAVRPSENFTNDYAIRAGVSESSVD 600
Qy	721 ETAQOLGLYYDTLKLSSVTSVADGTRALVEATLESACLSDLVHPENNATDVRYTT 780	Db	541 RNSAEKPDKOQETVFSVPDVGNNYGRDGEPPGVFAEAVRPSENFTNDYAIRAGVSESSVD 600
Db	721 ETAQOLGLYYDTLKLSSVTSVADGTRALVEATLESACLSDLVHPENNATDVRYTT 780	Qy	601 ETIVEMSYADMILKEASVTKLAAAGVAGIQLISLFSQYKFLKSSESSFORKDMVSSMESDVATI 660
Qy	781 RYEVFWSKSGWKITEGSVLAS .801	Db	601 ETIVEMSYADMILKEASVTKLAAAGVAGIQLISLFSQYKFLKSSESSFORKDMVSSMESDVATI 660
Db	781 RYEVFWSKSGWKITEGSVLAS .801	Qy	661 GSYRADDSSEALPRMDARTAENITYSKWQKIKSLAFLGPDHRIEMLPEVLDGRMLKIWTDRRA 720
RESULT 2		Db	661 GSYRADDSSEALPRMDARTAENITYSKWQKIKSLAFLGPDHRIEMLPEVLDGRMLKIWTDRRA 720
US-10-600-070-127	Sequence 127, Application US/10600070	Qy	721 ETAQOLGLYYDTLKLSSVTSVADGTRALVEATLESACLSDLVHPENNATDVRYTT 780
; CURRENT FILING DATE: 2003-06-20	; Publication No. US20040139500A1	Db	721 ETAQOLGLYYDTLKLSSVTSVADGTRALVEATLESACLSDLVHPENNATDVRYTT 780
; GENERAL INFORMATION:		Qy	781 RYEVFWSKSGWKITEGSVLAS .801
; APPLICANT: Osteryoung, Katherine W.		Db	781 RYEVFWSKSGWKITEGSVLAS .801
; APPLICANT: Vitha, Stanislav		RESULT 3	
; APPLICANT: Koksharova, Olga A.		US-10-600-070-129	
; APPLICANT: Gao, Hongo		; Sequence 129, Application US/10600070	
; TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of		; Publication No. US20040139500A1	
; FILE REFERENCE: MSU-08153		; GENERAL INFORMATION:	
; CURRENT APPLICATION NUMBER: US/10/600,070		; APPLICANT: Osteryoung, Katherine W.	
; CURRENT FILING DATE: 2003-06-20		; APPLICANT: Vitha, Stanislav	
; NUMBER OF SEQ ID NOS: 206		; APPLICANT: Koksharova, Olga A.	
; SOFTWARE: PatentIn version 3.2		; APPLICANT: Gao, Hongo	
; SEQ ID NO: 127		; TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of	
; LENGTH: 801		; FILE REFERENCE: MSU-08153	
; TYPE: PRT		; CURRENT APPLICATION NUMBER: US/10/600,070	
; ORGANISM: Arabidopsis thaliana		; CURRENT FILING DATE: 2003-06-20	
US-10-600-070-127		; NUMBER OF SEQ ID NOS: 206	
Query Match 99.7%; Score 4051; DB 4; Length 801;		; SOFTWARE: PatentIn version 3.2	
Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;		; SEQ ID NO: 129	
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		; LENGTH: 801	
Qy	1 MEALSHVGIGLSPQLCPCLPATTKLRSNTSTICASKWADRLLSDFNTSDSSSS 60	TYPE: PRT	
Db	1 MEALSHVGIGLSPQLCPCLPATTKLRSNTSTICASKWADRLLSDFNTSDSSSS 60	ORGANISM: Arabidopsis thaliana	
Qy	61 FATAATTATLVSLLPSTORPERHVPIDFYQVLAQTHFLTGIRAFEARVSKPPOFG 120	Query Match 99.7%; Score 4051; DB 4; Length 801;	
Db	61 FATAATTATLVSLLPSTORPERHVPIDFYQVLAQTHFLTGIRAFEARVSKPPOFG 120	Best Local Similarity 99.8%; Prd. No. 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	121 FSDDALISRRQILOAACETLNPRSRREYNEGLDDEBATTIDVPMNDKVPICALCVLQEG 180	Matches 799; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Db	121 FSDDALISRRQILOAACETLNPRSRREYNEGLDDEBATTIDVPMNDKVPICALCVLQEG 180	1 MEALSHVGIGLSPQLCPCLPATTKLRSNTSTICASKWADRLLSDFNTSDSSSS 60	
Qy	181 GETEIVLRVGEALLKERLPKSFQDVVLMALAFDVSRDAMALDPDFITGYBFVVEAL 240	1 MEALSHVGIGLSPQLCPCLPATTKLRSNTSTICASKWADRLLSDFNTSDSSSS 60	

US-10-600-070-131

Query Match 99.7%; Score 4051; DB 4; Length 801;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 2; Index 0; Caps 0;

Matches 799; Conservative 1; MEALSHVGIGLSPFOLCRPATTIKLRSSENTSTTICASKWADLLSDENFTSDSSSS 60

Db 1 MEALSHVGIGLSPFOLCRPATTIKLRSSENTSTTICASKWADLLSDENFTSDSSSS 60

Qy 1 MEALSHVGIGLSPFOLCRPATTIKLRSSENTSTTICASKWADLLSDENFTSDSSSS 60

Db 61 FATATTATLVSPLSPSIDRPERHYPIPDIFYQVLGAQTHFLTDGIRRAEARVSKPQFG 120

Qy 61 FATATTATLVSPLSPSIDRPERHYPIPDIFYQVLGAQTHFLTDGIRRAEARVSKPQFG 120

Db 61 FATATTATLVSPLSPSIDRPERHYPIPDIFYQVLGAQTHFLTDGIRRAEARVSKPQFG 120

Qy 121 FSDDALISRQILOACETISNPRSRRETEGLIDDEATVITDVKPGALCVLQEG 180

Db 121 FSDDALISRQILOACETISNPRSRRETEGLIDDEATVITDVKPGALCVLQEG 180

Qy 121 GETEIVLRGEALLKERLPKSFKDQDVLYMALAFDVSRAAMALDPDPTITGYEFVERAL 240

Db 121 GETEIVLRGEALLKERLPKSFKDQDVLYMALAFDVSRAAMALDPDPTITGYEFVERAL 240

Qy 241 KLLQEGASLAPDRLQIDETLEITPRYVLELLGLPGLDDYAAKRNLNGSGRNILWS 300

Db 241 KLLQEGASLAPDRLQIDETLEITPRYVLELLGLPGLDDYAAKRNLNGSGRNILWS 300

Qy 241 KLLQEGASLAPDRLQIDETLEITPRYVLELLGLPGLDDYAAKRNLNGSGRNILWS 300

Db 241 KLLQEGASLAPDRLQIDETLEITPRYVLELLGLPGLDDYAAKRNLNGSGRNILWS 300

Qy 301 VGGGASALVGGLTREKFMNEAFLRMTAAEQDLFVATPSNIPAESFEVYEVALVAQA 360

Db 301 VGGGASALVGGLTREKFMNEAFLRMTAAEQDLFVATPSNIPAESFEVYEVALVAQA 360

Qy 361 FIGKPHLJQDAKOFQOOLQAKQYNAMEIPAMLYDTRNWEIDFGLERGLCALLIGKVD 420

Db 361 FIGKPHLJQDAKOFQOOLQAKQYNAMEIPAMLYDTRNWEIDFGLERGLCALLIGKVD 420

Qy 421 CRMWLGDSBDSQRNPALTEFVLENSNDDNDLPGLKCLLLETWLAGVFPFRDTKDK 480

Db 421 CRMWLGDSBDSQRNPALTEFVLENSNDDNDLPGLKCLLLETWLAGVFPFRDTKDK 480

Qy 421 CRMWLGDSBDSQRNPALTEFVLENSNDDNDLPGLKCLLLETWLAGVFPFRDTKDK 480

Db 421 CRMWLGDSBDSQRNPALTEFVLENSNDDNDLPGLKCLLLETWLAGVFPFRDTKDK 480

Qy 481 KFKLGDDYDDPMVTLSYLERVEVYQGSPLAAATMARGHEVKASAMOALQKVFPSSRYTD 540

Db 481 KFKLGDDYDDPMVTLSYLERVEVYQGSPLAAATMARGHEVKASAMOALQKVFPSSRYTD 540

Qy 541 RNSAEPKVQETYSVDPVGNVGRDGFQGVFAEAURPSENFTNDYAIRAGYSESSVD 600

Db 541 RNSAEPKVQETYSVDPVGNVGRDGFQGVFAEAURPSENFTNDYAIRAGYSESSVD 600

Qy 601 ETIVEMSVADMILEKASVKTLLAAGVIAIGLISLFSQRYFLIKSSSFQKDMVSMESDVTI 660

Db 601 ETIVEMSVADMILEKASVKTLLAAGVIAIGLISLFSQRYFLIKSSSFQKDMVSMESDVTI 660

Qy 601 ETIVEMSVADMILEKASVKTLLAAGVIAIGLISLFSQRYFLIKSSSFQKDMVSMESDVTI 660

Db 601 GSYRADDSFALPMMDARTAENIVSKWQKIKSLAFCGDHRIEMLPEVLGMLKWIWDRAA 720

Qy 661 GSYRADDSFALPMMDARTAENIVSKWQKIKSLAFCGDHRIEMLPEVLGMLKWIWDRAA 720

Db 661 GSYRADDSFALPMMDARTAENIVSKWQKIKSLAFCGDHRIEMLPEVLGMLKWIWDRAA 720

Qy 721 ETIQQLVYDYLKLSSVTSVADGTRALVATELESSACLSLVHPENNATDVRYTT 780

Db 721 ETIQQLVYDYLKLSSVTSVADGTRALVATELESSACLSLVHPENNATDVRYTT 780

Qy 781 RYEVFWSKSGWKLTGEGSYLAS 801

Db 781 RYEVFWSKSGWKLTGEGSYLAS 801

Qy 661 GSYRADDSFALPMMDARTAENIVSKWQKIKSLAFCGDHRIEMLPEVLGMLKWIWDRAA 720

Db 661 GSYRADDSFALPMMDARTAENIVSKWQKIKSLAFCGDHRIEMLPEVLGMLKWIWDRAA 720

Qy 721 ETAGLGDDYDTLKLSSVTSVADGTRALVATELESSACLSLVHPENNATDVRYTT 780

Db 721 ETAGLGDDYDTLKLSSVTSVADGTRALVATELESSACLSLVHPENNATDVRYTT 780

Qy 781 RYEVFWSKSGWKLTGEGSYLAS 801

Db 781 RYEVFWSKSGWKLTGEGSYLAS 801

RESULT 4

US-10-600-070-131

; Sequence 131, Application US/106000070

; Publication No. US20040139500A1

; GENERAL INFORMATION:

; APPLICANT: Osteryoung, Katherine W.

; APPLICANT: Vitha, Stanislav

; APPLICANT: Koksharova, Olga A.

; APPLICANT: Gao, Hongo

; TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of

; TITLE OF INVENTION: Use

; FILE REFERENCE: MSU-08153

; CURRENT APPLICATION NUMBER: US/10/600,070

; CURRENT FILING DATE: 2003-06-20

; NUMBER OF SEQ ID NOS: 206

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 131

; LENGTH: 801

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

RESULT 5

US-10-739-930-5771

; Sequence 5771, Application US/10739930

; Publication No. US20040216190A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; TITLE OF INVENTION: NUCLEAR ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH

; PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-21 (5337) B

; CURRENT APPLICATION NUMBER: US/10/739, 930

CURRENT FILING DATE: 2003-12-18
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO 5771
 LENGTH: 801
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE: OTHER INFORMATION: Clone ID: ARATH-23APR03-C13643_1.p
 US-10-739-930-5771

Query Match Score 4051; DB 5; Length 801;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEALSHYGIGIISPFOLCRPLPATKLRSHNTSTTCSASKWADRLLSDFNFTSDSSSS 60
 Db 1 MEALSHYGIGIISPFOLCRPLPATKLRSHNTSTTCSASKWADRLLSDFNFTSDSSSS 60
 Qy 61 FATTATATLVSLLPSIDRPERHVPIDFYQVVLGAQTHFLTDGIRAFEARVSKPQFG 120
 Db 61 FATTATATLVSLLPSIDRPERHVPIDFYQVVLGAQTHFLTDGIRAFEARVSKPQFG 120
 Query Match Score 2926; DB 4; Length 578;
 Best Local Similarity 99.8%; Pred. No. 3..le-23;;
 Matches 577; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 79 RPERHVPIDFYQVVLGAQTHFLTDGIRAFEARVSKPQFGSSDDALISRQLQAAACE 138
 Db 1 RPERHVPIDFYQVVLGAQTHFLTDGIRAFEARVSKPQFGSSDDALISRQLQAAACE 60
 Query Match Score 2926; DB 4; Length 578;
 Best Local Similarity 99.8%; Pred. No. 3..le-23;;
 Matches 577; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 139 TLSNPRSRRENEYNEGLIDDEATATVITDWDKVPGALCVLQEGETEVILRGAEALKERL 198
 Db 61 TLSNPRSRRENEYNEGLIDDEATATVITDWDKVPGALCVLQEGETEVILRGAEALKERL 120..
 Qy 199 PKSFKQDYLVALAPLDVSRDMLALDPDFITGYFEVAL 240
 Db 121 PKSFKQDYLVALAPLDVSRDMLALDPDFITGYFEVALQEGASSLAPDLRQ 180
 Qy 241 KLIQEEGASSLADLRAQDITLEEITPRVYLELLGLPLGDDYAAKRNLGSVRNILWS 300
 Db 241 KLIQEEGASSLADLRAQDITLEEITPRVYLELLGLPLGDDYAAKRNLGSVRNILWS 300
 Qy 301 VCGGGASALVGGLTREKMPNEAFLRMTAAEQVQLFVATPSNIPAESPEVYEAVALVAQA 360
 Db 301 VCGGGASALVGGLTREKMPNEAFLRMTAAEQVQLFVATPSNIPAESPEVYEAVALVAQA 360
 Qy 361 FIGKCKPHLQLDAKQFQOLQOKXMANBIPAMLYDTANNNWFDFGLERGLCALLIGKVD 420
 Db 361 FIGKCKPHLQLDAKQFQOLQOKXMANBIPAMLYDTANNNWFDFGLERGLCALLIGKVD 420
 Qy 421 CRMWGLDSEDSQRNPNAIVEFYLENSRDRNDLPLGCLKLLETWILAGVVFPRFDTKD 480
 Db 421 CRMWGLDSEDSQRNPNAIVEFYLENSRDRNDLPLGCLKLLETWILAGVVFPRFDTKD 480
 Qy 481 KFKLGDDPMVLSYLERVEVYQGSPLAARATMARGAETHYKASAMQALQKVFPSSRYTD 540
 Db 481 KFKLGDDPMVLSYLERVEVYQGSPLAARATMARGAETHYKASAMQALQKVFPSSRYTD 540
 Qy 541 RNAAEPKDVOQETPSVDPVGNNGRQGPGVFTAEARPSNFETNDYAIRGVSESSVD 600
 Db 541 RNAAEPKDVOQETPSVDPVGNNGRQGPGVFTAEARPSNFETNDYAIRGVSESSVD 600
 Qy 601 ETTEVMYADMILKEASVRLKSLVTAAGVAGILISLFSQKYFLKSSSFQKDMVSSMESDVTI 660
 Db 601 ETTEVMYADMILKEASVRLKSLVTAAGVAGILISLFSQKYFLKSSSFQKDMVSSMESDVTI 660
 Qy 661 GSVRADDSEALPRMDARTAENIVSKWOKIKSLAFGPDHRIEMLPEVLDGRMLKIWTDRAA 720
 Db 661 GSVRADDSEALPRMDARTAENIVSKWOKIKSLAFGPDHRIEMLPEVLDGRMLKIWTDRAA 720
 Qy 721 EFAQLGLVYDYTLKLSDVTSVTSADGTRALVEATLESACSDLVPPENNATDVRTYT 780
 Db 721 EFAQLGLVYDYTLKLSDVTSVTSADGTRALVEATLESACSDLVPPENNATDVRTYT 780

RESULT 7
 US-10-600-070-125

Sequence 123, Application US/10600070
 Publication No. US20040139500A1
 GENERAL INFORMATION:
 ; APPLICANT: Ostryoung, Katherine W.
 ; APPLICANT: Vitha, Stanislav
 ; APPLICANT: Koksharova, Olga A.

Sequence 125, Application US/10600070
 Publication No. US20040139500A1
 GENERAL INFORMATION:
 ; APPLICANT: Ostryoung, Katherine W.
 ; APPLICANT: Vitha, Stanislav
 ; APPLICANT: Koksharova, Olga A.

RESULT 6
 US-10-600-070-123

APPLICANT: Gao, Hongo
 TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of Use
 FILE REFERENCE: MSU-08153
 CURRENT APPLICATION NUMBER: US/10/600,070
 CURRENT FILING DATE: 2003-06-20
 SEQ ID NOS: 206
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 125
 LENGTH: 760
 TYPE: PRT
 ORGANISM: Oryza sativa
 US-10-600-070-125

Query Match 43.7%; Score 1775.5; DB 4; Length 760;
 Best Local Similarity 4.9%; Pred. No. 4.4e-140;
 Matches 390; Conservative 119; Indels 93; Gaps 16;
 Qy 12 SPFQLCRPLPATTKURRSNTSTTC-SASKWADRLLSDFN----TSDSSSSSFATAT 65
 Db 14 APPAFSLPRRPRPRPRPPRPPHPSSACRAASRWAERLFAHDHLLPTAAPSDPPSPAPAPA 73
 Qy 66 TTATLVLSPPSIDRPERHYPIPDYQVIGAOTHFLTDGIRRAFEARYVSKPPQFGFSDDA 125
 Db 74 APSASFVFPVIFPDAERSLPLQDyEVKQGAEPHLGDPGIRRAFEARTAKPPQGYSTDA 133
 Qy 126 LISRQILQACETLSNPSSRENEGLDDEAATVITDPMKDVKPGALCVLOEGGETI 185
 Db 134 LVGRQMLQTAHDLMQNQNTQVDRALSEATLMDIAWDK-----EAGEALA 184
 Qy 186 VLRGEALLIKERLPLPKSFQDQVVLMAFLPDSRDAMALDPPDTITGTFVERALKLQE 245
 Db 185 VLTGEQLLIDRPPKRFQDQVVLAMALAYVLDLSRDAMASPPDVIGCEVLERALKLQE 244
 Qy 246 EGASSLAPDRLAQIDETLEBETIPTRVYLFLGLPLGDDYAAKRLNLGSCYRNILWSVGGG 305
 Db 245 DGASNLPADLSQIDETLEBETIPTRVYLFLGLPLGDDYAAKRLNLGSCYRNILWSVGRGG 304
 Qy 306 ASALVGGLTREKFNEAELRMTAAEQDVLFWATPSNIPASPEFYEVALLVAQAFIKK 365
 Db 305 IATVGGFSREAFKNEAFTMNTAAEQDVLFWATPSNIPASPEFYEVALLVAQAFIKK 364
 Qy 366 PHLIQDADKFOQFOOLQAKYMWIIPAMLYDTRNNWEIDFGFLERGLLIGKVDECRMWL 425
 Db 365 PQFIMMADDLFLQOKFNIGS---HYAIDN---EMDLAERAFCSLVGDVSKCRNWL 416
 Qy 426 GLDSEDSQYRNPAIVEFVLENS-RDDNDLPLGICKLKLFTWLTAGVVFPRFDTKKKFKL 484
 Db 417 GIDNESSPPRDPKILEFTIVNTNSSEENDLPLGICKLKLFTWLTIFEVPPRSRDTGMQFRL 476
 Qy 485 GDYDDPMVLSYLERVVQQSPLAANTMARIAGA-----HVKASAMQALQKVFP-SR 537
 Db 477 GDYDDPMVLSYLERVMEGGASHAAAIAKIGAQATTAALGTVKSNIAIQATNKVPLIE 536
 Qy 538 YDRENSAEPRDQVETVFSVDPVGVNNGRDGEPEGVFIAEVRSPENFNTDAIRAGYSES 597
 Db 537 QLDSAMENT-----KDG-PCGYL-----ENFDG-----559
 Qy 598 SVDETTVEMSVADMKEASVKILAAQVAGAILGSFLSQKYLKSSSFORKDMSSMSD- 656
 Db 560 -----ENPAHDSRNALKITISAGALFALLAVIGARY-----LPRKRPLSAIRSEH 605
 Qy 657 --VATIGSYRADSEAL-----PRDARTAENIVSKWOKISSLARGDHRIEMLPDEVL 707
 Db 606 GSTAVANVSDTODPALDEDPHIPRMDAKLAEDIVRKWQSIXSKSAGPEHSVASLOEVL 665
 Qy 708 DGRMLKIVTWDRAEATAOLGLYYDWTLLKLSVDSVTVSADGTRALVALTEESACLSLVIH 767
 Db 666 DGNLNLKWWTDRAEAEIERTGWFWYTLSDVTSRISITSLDGRATVEATIDEGQLTIVTE 725
 Qy 768 PENNADVRYTTRYFWSK-SGWKITEGVSYLAS 801
 Db 726 PRNNDSYDTKTYTRYEMAPSILGGWKTETGAVLK 760

RESULT 8
 US-10-600-070-206
 Sequence 206, Application US/10/600,070
 Publication No. US20040139500A1
 GENERAL INFORMATION:
 APPLICANT: Osteryoung, Katherine W.
 APPLICANT: Vitha, Stanislav
 APPLICANT: Koksharova, Olga A.
 APPLICANT: Gao, Hongo
 TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of Use
 FILE REFERENCE: MSU-08153
 CURRENT APPLICATION NUMBER: US/10/600,070
 CURRENT FILING DATE: 2003-06-20
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 206
 LENGTH: 324
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-600-070-206
 Query Match 40.5%; Score 1646; DB 4; Length 324;
 Best Local Similarity 100.0%; Pred. No. 9.3e-130;
 Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEALSHVGIGLSPSPFOLCRLPATTKLLRSHTNTTCSASKWADRLLSDFNTSDSSSS 60
 Db 1 MEALSHVGIGLSPQLCRLPATTKLLRSHTNTTCSASKWADRLLSDFNTSDSSSS 60
 Qy 61 PATTTTATLVSLLSPSIDRPERHYPIPDYQVIGAOTHFLTDGIRRAFEARTVSKPQFG 120
 Db 61 FATTATTATVSLSPSIDRPERHYPIPDYQVIGAOTHFLTDGIRRAFEARTVSKPQFG 120
 Qy 121 FSDDALISRQILQAACTLSNPSSRENEGLDDEAATVITDPMKDVKPGALCVLQEG 180
 Db 121 FSDDALISRQILQAACTLSNPSSRENEGLDDEAATVITDPMKDVKPGALCVLQEG 180
 Qy 181 GETEIVLVRGEALLKERLPLKSFKDQVVLMAFLDVSRSRDAEALDPPDFITGYFVEEAL 240
 Db 181 GETEIVLVRGEALLKERLPLKSFKDQVVLMAFLDVSRSRDAEALDPPDFITGYFVEEAL 240
 Qy 241 KLLQEBGASSLAPLRAQDETLEBETIPRVYLELLGPLGDDYAAKRLNLGSYRNILWS 300
 Db 241 KLLQEBGASSLAPLRAQDETLEBETIPRVYLELLGPLGDDYAAKRLNLGSYRNILWS 300
 RESULT 9
 US-10-600-070-122
 Sequence 122, Application US/10/600,070
 Publication No. US20040139500A1
 GENERAL INFORMATION:
 APPLICANT: Osteryoung, Katherine W.
 APPLICANT: Vitha, Stanislav
 APPLICANT: Koksharova, Olga A.
 APPLICANT: Gao, Hongo
 TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of Use
 FILE REFERENCE: MSU-08153
 CURRENT APPLICATION NUMBER: US/10/600,070
 CURRENT FILING DATE: 2003-06-20
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 122
 LENGTH: 525
 TYPE: PRT
 ORGANISM: Oryza sativa

RESULT 10

US-10-600-070-122

Query Match Score 32.8%; Score 1332; DB 4; Length 525;
Best Local Similarity 48.8%; Pred. No. 5. 9e-103;
Matches 287; Conservative 88; Mismatches 137; Indels 76; Gaps 11;

Qy 81 BRHVIPIDFQVLGAOTHTFLTDGIRAFERARSKEPQFGFSSDDALISRRQIQLQACETL 140
Db 3 ERSPLQVDFTKVKLGAEPHFGDGIERRAFERARIAKPQYGSSTDALVGRRLMQLQIAHDTL 62

Qy 141 SNPRSRREYNGLDDEBATVITDVPWDKVPGCALCIVLQEGERETEIVLVRGVALLKERLPK 200
Db 63 MNQNSRTQYDALSSENREALTMDIADWK-----EAGBALAVLTGEQLLDRPK 113

Qy 201 SPKDQVYLVMALAFDVSRDAMALDPDPDFITGYEFYEBALKLLOEQGASSIAAPDLRAQID 260
Db 114 REKQDVYLAMVLAAYDLSRDAAMAASPPDVTCSCCEVLERALKLLOEQGASNLAPDLISQID 173

Qy 261 ETLEETIPTRVYLELLGLPGLDQDYAARLNGLSGVRLTILWSGGGASALVGGLTREKFMN 320
Db 174 ETLEETIPTRVYLELLSULPIDEHHHKRQEGQ.GARNILWSGRGGIATVGGFSRSEAFMN 233

Qy 321 EAFLRMTAAEQQVLDFYATPSNIPAESFEVVEYEAVALVAQATIGKPKHLLQDADKQFOQQLQ 380
Db 234 EAFLRMTSIEONDFFSKTPNSIIPPENFEVYNAVALAHAQATISKRFQIMADDLFEQLQ 293

Qy 381 QAKWMAAMEIPAMLYDPFRNNWEDFGELRGCLCALLIGKYDPRMWLGLDSESQYRNPAIV 440
Db 294 KENIGS---HYAYDN---ENDLALERAFCSLLVGDVSCKRMWLGDNEESPYDPKIL 345

Qy - 441. EFPVLENS-RDDNDLFLGLCLKLETLAGVYPERFDTDKRKFKLQGDDYDPMVSYLER. 499

Db 346 EPIVINSISBENDLFLGLCLKLETLIFEYPRSDTRGMQFRLGDDYDPDEVSYLER 405

Qy 500 VEVVOQSPSLAAATAATMARGAE-----HVKASAMOALQKYPF-SRYTDRNSAEPKDVQET 552
Db 406 MECCGASHLAAAATIAKLGQDATAALGTVRKNAIQAFNKVPLIEQUDRSAMENT----

Qy 553 VFSVDPVGNVNGRGEPEGVFAEAVERPSENFTNDVIAVAGYSESSVDETTEVMSVADM 612
Db 461 -----KDG-PGGYL-----ENPDQ-----ENAPAHDS 481

Qy 613 RGAASVKAIIAAGVAIGLISLFLKSSSSFQRKDVMSSMESDVATI 660
Db 482 RNAALKISAGALPALLAVIGAKY-----LPRKREPLSARSEHGSV 522

RESLT 10 US-10-424-599-271849

Sequence 271349, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plant Improvement
; FILE REFERENCE: 38-21532231 B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 271849 LENGTH: 344
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_87499C.1.pep

Query Match Score 32.8%; Score 1332; DB 4; Length 525;
Best Local Similarity 48.8%; Pred. No. 5. 9e-103;
Matches 287; Conservative 88; Mismatches 137; Indels 76; Gaps 11;

Qy 16 LCRLPATT-----KURRS--HNTSTTICSAKWNADRILSDNFNTDSSSSPATATT 66
Db 12 LCTPHPTTTHPTPKPNQNLRLSSRGASLSATSCKWAERLIADFQLGDAAS--TSTS 68

Qy 67 TATLVSPSPSIDPERHPVPIPDPYDQVQGAQTHFLTGIRAFEARVSKPPQQTGFSDDAL 126
Db 69 TLSPPSPRPLDPPERVSVIPDLYRLIGAEPHFLGDIRRAYAKFSKPPQTAFSNDAL 128

Qy 127 ISRQIQLQACETLNSNRSSREYNEGLDDEBATVITDVPWDKVPGALCVLQERGETEV 186
Db 129 ISRQIQLQACETLADTSRRETNQSLVDEBAILTQIPDVKPGALCVLQERGETEV 188

Qy 187 LRVGEALLKERLPKSFQDQVYVLMALAFDVSRDAMALDPDPDFITGYEFVEEALKLQQE 246
Db 189 LEIQQGILRERLQPKTFQDVVIALMFVDSRDAMALSPDPDFTAACMMLERAIKLQQE 248

Qy 247 GASSLAPDLRQIQTETEETIPTRVYLELLGLPGLDQDYAARLNGLSGVRNILMSVGSSA 306
Db 249 GATSLAPDLQIQTETEETIPTRVYLELLGLPGLDQDYAARLNGLSGVRNILMSVGSSA 308

Qy 307 SALVGGITREKEMNEAFLTRMTAAEQVLFVATPSNI 342
Db 309 ATTARGFTREDPMNEAFLHMATAEQLFLVATPSNI 344

RESLT 11 US-10-425-115-266516

Sequence 266516, Application US/10425115
; Publication No. US200401427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Other Molecules
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21532221 B
; CURRENT APPLICATION NUMBER: US/10/425, 115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 266516 LENGTH: 364
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE: OTHER INFORMATION: Clone ID: MRT4577_174665C.1.pep
US-10-425-115-266516

Query Match Score 23.9%; Score 973; DB 4; Length 364;
Best Local Similarity 54.8%; Pred. No. 5.9e-7;
Matches 198; Conserved 54; Mismatches 79; Indels 30; Gaps 4;

Qy 12 SPFOLCPUPPATKLRSHT---STTICSAKWNADRILSDNFN-----TSDSS 57
Db 14 APFAFSPPIP-----LRSHRPPPPGPSTCRANSWRFLFADFLLLAAADPPAAASSSS 68

Qy 58 SSSPATATTATLVSLLPSIDPERHPVPIPDPYQVQGAQTHFLTGIRAFARVSKEP 117
Db 69 SSPP-----VTPPEADRALPLPDPYKLGABPHFLGDIRAFSRIAKEP 117

Qy 118 QGFPSDDALISRSRQLQACETLNSNPSRREYNEGILLDDEATVITDWDKVPGALCVL 177
Db 118 QYGSTEAFLVGRQMLQIAHDTLTNQSRTETDRALESDRDALTMWDKVPGVLCV 177

Qy 178 QEGGETEVRLGEALKERLPKSFQDQVYVLMALAFDVSRDAMALDPDPDFITGYEFV 237
Db 178 QAGEAQIVLANGEHLLQDRPKFQDVVLMALAVDIRDAMAASPPDVICCCVEILE 237

Qy 238 RAFLKLIQEGASLAPLQDRAQIDETEETIPTRVYLELLGLPGLDQDYAARLNGLSGVRN 297
Db 238 RAFLKLIQEGASNLAPLQDRAQIDETEETIPTRVYLELLGLPGLDQDYAARLNGLSGVRN 297

US-10-600-070-167
; Sequence 167, Application US/10600070
; Publication No. US2004139500A1
; GENERAL INFORMATION:
; APPLICANT: Osteryoung, Katherine W.
; APPLICANT: Vitha, Stanislav
; APPLICANT: Koksharova, Olga A.
; APPLICANT: Gao, Hongbo
; TITLE OF INVENTION: Plastid Division and Related Genes and Proteins, and Methods of
; FILING DATE: 2003-06-20
; CURRENT APPLICATION NUMBER: US/10/600,070
; NUMBER OF SEQ ID NOS: 206
; SEQ ID NO: 167
; LENGTH: 768
; TYPE: PRT
; ORGANISM: *Nostoc punctiforme*
; SOFTWARE: PatentIn version 3.2
; CURRENT FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 206
; SEQ ID NO: 167
; LENGTH: 768
; TYPE: PRT
; ORGANISM: *Nostoc punctiforme*
; US-10-600-070-167

Query Match 12.9%; Score 524.5; DB 4; Length 768;
Best Local Similarity 24.9%; Pred. No. 1.2e-34;
Matches 212; Conservative 128; Mismatches 286; Indels 227; Gaps 28;

Qy 84 VPIPIDPVQVGAQTHFLTDTRRAFARVSKPPQPGFSDALISRQILQAACTELSNP 143
Db 1 VRIPLDYRIGLPLAAEQQDQRQASDRITQLPREYSSQAAISSRQLIBAYVVLSDP 60
Qy 144 RSRREYNEGLL-----DDEBATVIT-----DVPWDVPGALCVLQ 178
Db 61 KQRSTVDQLYAHAYDPDNLAAAQAQENRTESTKRGSDTQSLGIEITQDIBLVGALLQ 120
Qy 179 EGGETEVLRVEBALL--KERIPLPKSFQ----DYLWMLAFLDYSRD- 220
Db 121 EGEYEYLVKLGERPLWKNSGATSSRSXSNNLADEEIVYESAHPDVLTVAACLEGRBQ 180
Qy 221 -----AMALDPPDFITGYEVFEEALKLQOEGRASSLAIDLRAQIDETLBEITPRVY 271
Db 181 WOGHYNAAFILE-----TGQE-----LIVREG---LFSISIQAEIQADLYKLERPYI 225
Qy 272 LEILGPQGDYAAKRINGLGSYRNILWSVGG--GGASALVGSLTRB--KFMNEAFIRMT 327
Db 226 JELLALP--QEKTAERSQGLLEQNLLLEDRGSGIDGTNIDDEFILRFIQLQRNHT 283
Qy 328 AAEQDQDIFVATPSNIPASFEYEAVALVAGKPAQFOOLQQAKWMAM 387
Db 284 VAHQHKLFEAQSKR--SSAVATYLAVVALIARGFAQRQMLVRIGKQ--- 337
Qy 388 EIPAMLYDTTRNNWEIDFGLERCLCALLIGKVDECRMWGLDSEDSQYRNPAIVEFLENS 447
Db 338 -----DVLHEQSICLALLGOTEEATRYLESQE---YE---ALAFIREKS 376
Qy 448 NRDDNDLPLGCKLLETLWLAGVFPFRPTDIDKKFKLQGDDYDPMVLSYLRLRVEVVQGSP 507
Db 377 -QDSPDLIPGLCILYABOWLQEVPHFRDLANQQAFLKYFANQVOAYLSE-----426
Qy 508 LAAATMARIAGHEVKASAMOALQKVPSRVTDRNDAEKF-----DVOETYFSV 556
Db 427 -ALPTDQTTNEWAVINPQFPOKAQAKNTHPHNNSTKTSFNFHNSRPNPPLPET----480
Qy 557 DPVGNVNGRGEPEGVFTAEARVPSENFTNDYAIRGVSESSVDETTVEMSYADMILK--
Db 481 -----PTK--ETSETPNFSPMSSGSGTKESEPAERMRSGT 516
Qy 614 ---EASYKILAG-----623
Db 517 NOHLNGSAKSAAASGHNQKRRRKPTPSASRERIPDNRPHSSRRRTFANTIEGKTRLV 576
Qy 624 --VAIGLISL-----669
Db 577 WRVFISLVSILVFWLATTTFGMWLKNLFFPQPSPDPLQLFVQINQPPLPIPDPNRKESE 636

RESULT 15
US-10-424-599-177901
; Sequence 177901, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalcic David K
; APPLICANT: Zhou Xihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION: US/10/424, 599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO: 177901
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_131660C.1.pep
; US-10-424-599-177901

Query Match 12.3%; Score 499; DB 4; Length 204;
Best Local Similarity 51.2%; Pred. No. 2.1e-33;
Matches 104; Conservative 39; Mismatches 58; Indels 2; Gaps 2;

Qy 601 ETTEVEMSYADMILKEASYKILAAQVAIGLISLFSQKYF-LKSSSSFORKDMVSSMESDVAT 659
Db 2 ETRKGVFTIEEIKHASTQIMCAVGIVLTVGLKFLPTRNGSPILRKMTGSAVSDTIN 61
Qy 660 IGSVRADDIS-EALPRMARTAANI VSKWQKIKSLSAFLGDPDHR EMLPEVLDGMUKIWTRD 718
Db 62 LGSLGDEEKEVQLPKMDARVAALVTKWQSVKSEAEPDHCLGRLHEVLDGEMLKWTDR 121
Qy 719 AAETAQOLGLVYDXTLKLISVDSVTVAAGTRALVEATEESACLSLVLHPPENNATDVTY 778
Db 122 AEIAEABRGWSYDTITLEUNIDSVTISONGRRAVETTLEKESTHNAVGPQHDASNSRY 181

Search completed: December 4, 2005, 12:12:30
Job time : 170 secs

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OM protein - protein search, using SW model

Run on: December 4, 2005, 12:29:10 ; Search time 11 Seconds
(without alignments)
348.678 Million cell updates/sec

Title: US-10-600-070B-2

Perfect score: 4063

Sequence: 1 MEALSHVGICLSPFPQLCRILP.....YEVFWKSGWIKTEGSVILAS 801

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:
 1: /cgn2_6_ptodata/1/pubpaas/US09_NEW_PUB.pep:
 2: /cgn2_6_ptodata/1/pubpaas/US06_NEW_PUB.pep:
 3: /cgn2_6_ptodata/1/pubpaas/US07_NEW_PUB.pep:
 4: /cgn2_6_ptodata/1/pubpaas/US08_NEW_PUB.pep:
 5: /cgn2_6_ptodata/1/pubpaas/PCT_NEW_PUB.pep:
 6: /cgn2_6_ptodata/1/pubpaas/US10_NEW_PUB.pep:
 7: /cgn2_6_ptodata/1/pubpaas/US11_NEW_PUB.pep:
 8: /cgn2_6_ptodata/1/pubpaas/US60_NEW_PUB.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	116	2.9	1448	6	US-10-485-517-212	Sequence 212, App
2	111.5	2.7	3704	6	US-10-513-786-1	Sequence 1, App
3	109.5	2.7	661	6	US-10-467-657-1266	Sequence 1266, App
4	107	2.6	908	6	US-10-467-1070	Sequence 1070, App
5	105.5	2.6	817	6	US-10-793-626-50	Sequence 50, App
6	105.5	2.6	817	6	US-10-793-626-1528	Sequence 1528, App
7	104.5	2.6	402	6	US-10-858-730-30	Sequence 30, App
8	104	2.6	627	6	US-10-467-657-5432	Sequence 5432, App
9	103.5	2.5	715	6	US-10-467-657-70	Sequence 70, App
10	103.5	2.5	715	6	US-10-467-657-3672	Sequence 3672, App
11	103.5	2.5	2004	6	US-10-467-657-84	Sequence 84, App
12	103.5	2.5	2004	6	US-10-467-657-6322	Sequence 6322, App
13	103	2.5	565	7	US-11-074-176-98	Sequence 98, App
14	101	2.5	403	6	US-10-858-730-27	Sequence 27, App
15	101	2.5	711	6	US-10-467-657-2966	Sequence 2966, App
16	100.5	2.5	1663	6	US-10-982-545-6	Sequence 6, App
17	99	2.4	943	6	US-10-467-657-5508	Sequence 5508, App
18	98	2.4	611	7	US-11-082-389-436	Sequence 436, App
19	97.5	2.4	505	6	US-10-467-657-5148	Sequence 5148, App
20	97.5	2.4	791	6	US-10-467-657-5014	Sequence 5014, App
21	97.5	2.4	1192	6	US-10-858-730-72	Sequence 72, App
22	96.5	2.4	724	6	US-10-793-626-3082	Sequence 3082, App
23	96.5	2.4	1152	7	US-11-055-822-308	Sequence 308, App
24	95.5	2.4	566	6	US-10-467-657-3302	Sequence 3302, App
25	94.5	2.3	1020	6	US-10-513-786-4	Sequence 4, App

RESULT 1
US-10-485-517-212
; Sequence 212, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P10629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIOR APPLICATION NUMBER: GB 0200349,9
; CURRENT FILING DATE: 2004-02-02
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349,9
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 212
; LENGTH: 1448
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-485-517-212

RESULT 1
US-10-45-517-212
; Sequence 212, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P10629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; PRIOR APPLICATION NUMBER: GB 0118825,9
; CURRENT FILING DATE: 2004-02-02
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349,9
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 212
; LENGTH: 1448
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-45-517-212

Query Match 2.9%; Score 116; DB 6; Length 1448;
Best Local Similarity 19.4%; Pred. No. 0.52; Indels 220; Gaps 33;
Matches 134; Conservative 103; Mismatches 234; Query 151 EGLIDDEATVTIDPVDPKVPGALCVQEGGETRIVYGEALLKERLPKSFKDQDVLYM 210
Db 415 QGTTAD--TTKTDVADBL---ATKANEKQALIAQTADATTEKEAQANQQDAQLTQ 466
Db 415 QGTTAD--TTKTDVADBL---ATKANEKQALIAQTADATTEKEAQANQQDAQLTQ 466
Query 151 EGLIDDEATVTIDPVDPKVPGALCVQEGGETRIVYGEALLKERLPKSFKDQDVLYM 210
Db 415 QGTTAD--TTKTDVADBL---ATKANEKQALIAQTADATTEKEAQANQQDAQLTQ 466
Db 522 N----NETTNREKGNDIGPVRAAYEEELNNI----NAATTGDTYTAK-----561
Db 467 GNQNIE--NAQSTD--DVNTAKDNAIQADPIQASTDVTKNARAEELLTEMONKITEILN 521
Db 562 -DPAVQKQQLHANPKPGK-----LQQAADDKTQIBQTPNQASQEQINDAK- 611
Query 325 RMTAAEQTDLFVATPSNIPAESPEVVEYALVYQAFIGKKPHLQDADQFOOLQOQAV 384
Db 562 -DPAVQKQQLHANPKPGK-----LQQAADDKTQIBQTPNQASQEQINDAK- 611
Query 365 MAMEIPAMLYDTRNNWEDPGLERGLCALLIGKVDECRMWLGLDSESDQRNPAIVEFVL 444
Db 612 --QBVDTTELNOQAKTN-----VHQ-----SSTNEYVDNAVK-----640

ALIGNMENTS

Qy	445 ENSNRDDDDLPGLCKLLETLWLAGVVPPRERDTKKEFKLGDYDDEPMVLSTLERVEVQQ	504	Qy	282 DIAAKRNLGSGYRNLLMSVGCGASALVGGLTREKF--MNEAFLRMITAEQV-----	332
Db	641 -----GKAKI----NAVKTFSEYK--KDALAKIEDAYN-----AKVN 671		Db	2024 --QCHKVTHINFVPSML-----HAMILQALDBKDFAIMNRKLYTIVAGEANSPELCNR 2073	
Qy	505 GSPLAAATMARI.GAETHYKA-SAM-QALOKVPSRTDNRSAEPAKDVQBTVFSDPVGANNVG 564		Qy	333 -----DLFVATPSNIAESFEVYEVALVAQAFIGKPKPHLQDADKOFQOLQQ 381	
Db	672 EADNNASTSSEL-----AEAOKLAELKQTAQDNVNOATSKDDIEVQINNDL-DNI- 722		Db	2074 LYAHCPNVKLENLYGPTEGTIVATGFSIHKE--MNANVNPIGK-----PLSH 2118	
Qy	565 RDGPBPVGFIAEVRPSENFTEDYIAAGVSESSV-----DET 602		Qy	382 AKYNAMEIPAMLYDTRNNWEIDGLGLERIC--ALLIGK-----VDECRMWGLDSED 431	
Db	723 -----NDTIPGKRESATTDLIYADQKKNNTISADTNQDEK 761		Db	2119 VETYLID-----LENSNRDDND-----DLPGLCKLLETLWLAGVFPFRFD 476	
Qy	603 TVEMSVADMILKEASVKLIAAGVAGLISLSQKYFLKSSSFORKOMVMSMESDVATIG- 661		Qy	432 SQYRNPAIVEFV---LENSNRDDND-----DLPGLCKLLETLWLAGVFPFRFD 476	
Db	762 QQAQKVDQNQVPALESINNGYDNGDV-----DDAIIQGKAAIDAIQVD-AFVKP 810		Db	2171 RMYRTGDLVRLWDGNIEYLGRIDNQVKIRGFRIBLEGTEAAIAALEDVQTV-TTMID 2229	
Qy	662 -----SYRADDS-EALPRMDARTAENIVSKMOKIKSLAFGPDPHRLEMPLPEVLDGRMLKI 714		Qy	477 TKDKK-----FKLGDDYYDPPMVLSYLERVYVQGSPLAAAATMARIGAETHVKASAMQL-- 530	
Db	811 KANOATEKVAEKTKESTDQDQITAE-----EKTEALA-----MIKQITDOAKQGI 856		Db	2230 HKGANKTVAYVSEKYE-----ERIR-----EHVKKCTL.PQYMVP 2264	
Qy	715 WTDRAAETAAOL-----GLVYDYLKLISVSDVTWAD---GTRALVEATLEE 758		Qy	531 -----QKVUPP-----SRYTDRNSAEPKDVQESTVFSVYDPMGNVGRDGEPGVYFIAEVAPRSEN 582	
Db	857 -TD-ATTAAVEKAAGCQLEAPDNIQDSTEKOAIELETALDQIEAGVNVNADATTE 914		Db	2265 SYFVSMKALPLNKGKVDRKQHLHSVYBTSMDTVIVSPRNKEAMLSV-IWQBELGLEN 2323	
Qy	759 -----SACSLDLYHPENNAT-DVRYTYTTRYEV 784		Qy	583 FETNDYAIRAG-----VSE-----SSDDETTVEMSVADMILKEASVKIL-A 621	
Db	915 KEAFTALEDIL---SKATEDISQTTNAEI 942		Db	2324 ISVHDNFFPKLGKHSINATOLVSKYSCVRVMPLKQVFOYTTLATMARYLIELLVSAYDE 2383	
<hr/>					
RESULT 2					
US-10-513-786-1					
; Sequence 1, Application US/10513786					
; GENERAL INFORMATION:					
; APPLICANT: Bio Control Institute Limited					
; APPLICANT: OHTA, Michio					
; APPLICANT: AGATA, Norio					
; TITLE OF INVENTION: A cerulide synthetase, a gene thereof, and a detection method for					
; TITLE OF INVENTION: cereulide.					
; FILE REFERENCE: P0202401					
; CURRENT APPLICATION NUMBER: US/10/513,786					
; CURRENT FILING DATE: 2004-11-16					
; PRIOR APPLICATION NUMBER: JP P2002-142398					
; PRIOR FILING DATE: 2002-05-17					
; NUMBER OF SEQ ID NOS: 21					
; SOFTWARE: PatentIn version 3.1.					
; SEQ ID NO 1					
; LENGTH: 3704					
; TYPE: PRT					
; ORGANISM: Bacillus cereus					
US-10-513-786-1					
Query Match	2.7% ; Score 111.5; DB 6; Length 3704;		Query Match	2.7% ; Score 109.5; DB 6; Length 661;	
Best Local Similarity	19.4%; Pred. No. 5; Mismatches 301; Indels 241; Gaps 36;		Best Local Similarity	19.7%; Pred. No. 0.48; Mismatches 185; Indels 179; Gaps 28;	
Matches 159; Conservative			Matches 108; Conservative		
Qy	105 TIRAFEARVKPPQFGFDDALISR-ROILQAETISNPNSRRENEYGLJLDBEATIT 163		Qy	204 QDV-VLMALAFIDVSRDAMAL-----DPPDFITVYEFVSBALKLQB 245	
Db	1797 IHELFEAHVHTP---SATALLYRNKEMTYEDVNAQANALAHKLDRAGVGNQVWVL 1852		Db	1911 GENFYLDARLPEGDRDLQINNPNPTNLAYIYTSGSTGNPKGMVMAHQSVNLLDQE 1970	
Qy	164 DVPMWKVPGALCVLQEGG-----ETEIVLRGEA-----LLKERLPKSFK 203		Qy	246 EGASSLADLRAQIDETUEITPRYVRLGLPLGDDDYAAKRUNGLSGYRNILMSVGEGG 305	
Db	1853 DRSPFMVGLAVLKAGGAYLPIDTAYMORTYVQNSETILLTKCYLRESL--DFE 1910		Db	1971 K-YPVLAEDKHLKTTYTFDVSVAIEGWFHAGGLVIAHHGDEKOPKLQI-----NYISDGHNGDFSIIGEGA 267	

306 ASALV----GGLTREKFMN-----EFLRMTAAEVDLFV----ATPSNIPAESF 347
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 268 AFALTWLEGGSCANESYYNUILPTSILGGTHEAGLKOAVENAVNNPNTNLHULPRGVQSD 327
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 348 EVY-EVALALVAQAFIGKEPHILQDADKFQOLOQAKYNAME---IPAMLYDTRNNW - 400
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 328 DVFGKTAFTVLSARVL----DPOQGQTIXDKLTNRDAKLVAASGDPLELWLN 376
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 401 -EIDFG-----LER----GCLALIGKVDECRMWLGLOSDSDQXR 435
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 377 QNVDFGKKAELAELAIRQAQAIRSYKKEKRGKSGV-AILPGKLTDCC----ESEDIREN 429
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 436 NPAIIVEPVILENSNEDDDILPGLCKLLETLW----LAGVVPERFRDTKDRCFKLGDYV 488
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 430 ELFVE----GDSAGGSAKLARDKATQAILPLRGKVLNSPEVHPDOLFGNAETH 479
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 489 D-----DPMVLISYLERYBVEVQGSPLAAAATMARIAGAEHKVASKAMOALQKVPPSRYTDR 541
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 480 DISVAVGVDPAINDHPDLSGLRGKIAITSD-ADVGDSHIIQVILLTLPRHFPLKLVADG 538
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 542 N-SAEPKDQVETYPSVDPVGNNGRDEGPGVFAEAVRPSENPETDYAIRGVSESSV 599
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 539 HIXYAAP----PLFRVD----VNAQGRKS-----KPARKE----YAL-----567
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 600 DETTVEMSVADMKREASVKKLAAGVAGLISLRFQKYFLKSSSFQRKDMVSSMNEDEVAT 659
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 568 DONELD-GILERLQKEGVKETAYSI-----SRPKGLGENMDQLKD-TTMHPDTR 616
 Qy :|:||:|:||:|:||:|:||:|:||:|:
 Db 660 IGSVRADDSEALPRMDARTAENIVSKWQKIKSLAFLGPDHRITEMPEVLDGMRMLKIWTDR 719
 Qy :|:||:|:||:|:||:|:||:|:||:|:
 Db 617 LLQQQIPEPS----ADDETDRIFVKLMGKGEAA-----RRAMMERE 653
 Qy :|:||:|:||:|:||:|:||:|:
 Db 720 AETRQLGL 727
 Qy :|:||:|:||:|:||:|:
 Db 654 GDTAQQLDI 661
 Qy :|:||:|:||:|:
 RESULT 4
 US-10-467-657-1070
 ; Sequence 1070, Application US 10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FONTANA SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO: 100
 ; LENGTH: 908
 ; TYPE: PPT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-1070
 Query Match 2.6%; Score 107; DB 6; Length 908;
 Best Local Similarity 19.3%; Prod. No. 1..2; Mismatches 250; Indels 286; Gaps 37;
 Matches 154; Conservative 108; Mismatches 250; Indels 286; Gaps 37;
 Qy 143 PRSERREYNEGGLDDEEAT----VITDVWPDVKVPGALCVLQEGGE--TBIVLRVGE---191
 Db 62 PDDLRPQAELPDVLVRLTGWPVVLVIGQVEADDVIGTLA-KKQAEHGLRVIVSTGKDMA 119
 Qy 192 ALJKEERLPKFSKQDODVYLVNALAPLDSV-----RDAMAL--DPPDFITGEBFV 236
 Db 120 QLVDERV----TLVNTMSGETL DIEGVKAKEFGVRPQDQIRDYLALIGKDVNPGVBEKC 173
 Query Match 2.6%; Score 105.5; DB 6; Length 817;

Qy 237 --EEALKLLOB---EGASSLAPDLRAQIDETLEETTPRYVL--EILGLPLODDYAAKRL 288
 Db 174 GPKTAWKWLAEYGSLQGVMEHAPEIKGVGENLQALPQLPLSYDLYTICKDVDLTELS 233
 Qy 289 NGLSGYR-----NILWSVGGGAGASALVGG 3.13
 Db 234 DGIESIRRATPKWAQIAVDPKRWGFRTWLKEAESNNNTGSTDDLRGSDSIGEQAAANAEI 293
 Qy 314 TREKPMNEAFLRMTAAEQLDVFAT-----PSNIPAESPEVY 350
 Qy :|:||:|:||:|:||:|:||:|:||:|:||:|:
 Db 294 PSEKRAKA---TAPEKLDYQAVTTEAQAFAALLDKLAKADTIGIDTERTSLDAMNAELV 349
 Qy :|:||:|:||:|:||:|:||:|:||:|:
 Db 351 EVALLA-----QAFIGK-KPHLQDADQFQOLQOQAKYNAME 388
 Qy :|:||:|:||:|:||:|:||:|:
 Db 350 GISIAFQAGEAVYI PWGHSLTAAPQDQLQDVLGRKPHLENPALKKIGQ-----399
 Qy 389 IPAMLYDTR----NNWEIDFGLERGLCALLJGK-YDECRLMWLGLD-----428
 Qy :|:||:|:||:|:||:|:||:|:
 Db 400 --NLYKDQHYFANYGIALNNIAGDAMALASYTIESHIGHGLDBLSGRWLGLBTITYBSLCG 457
 Qy :|:||:|:||:|:||:|:
 Db 429 --SEDSQYRNPAI---VVFYLENSRDDNDLPLGCKLLETWLAGVTFPRRDTKDKKPK 483
 Qy :|:||:|:||:|:||:|:||:|:
 Db 458 KGAKQISIPDAVIAQGATEAAQDAD----FALRLEARLRA----QMDDKQLE 501
 Qy :|:||:|:||:|:||:|:
 Db 484 LGDYDYPWYLPSYL-RVEVYQGSPLAAAATMARGAHEHYKASAMOALQKVPSRVTDRN 542
 Qy :|:||:|:||:|:||:|:
 Db 502 MYERMLPLVQAQLPMECNGVQIDRAELAROSAELGAELMKLE---QEAYAARGOPFN 556
 Qy 543 SAEPKDQVETYPSVDPVGNNNGRDGEPGVFTAEEAVRPSENFETNDYAIRGVSESSVDET 602
 Qy :|:||:|:||:|:||:|:
 Db 557 LNSPQLQELTF--DRMG-----TAKGGISTN-----589
 Qy :|:||:|:||:|:
 Db 603 TVENSVADMILKEASVKKILAGVAIGLISLPSQKYP_LKSSSSFORKDMVSSMESDVAT-- 659
 Qy :|:||:|:||:|:
 Db 590 -----EAVLEQALADYPLPKIIQNRSLAALKSTYTDKLFEMISP RDNRHTTY 638
 Qy :|:||:|:||:|:
 Db 660 -----IGSVRADDSSEALPRMDARTAENIVSKWQKIKSLAFLGPDHRLEMPLPEVLDGMMLKI 714
 Qy :|:||:|:||:|:
 Db 639 AQAVAITGRLASNNNNPNLQNPIRTA-----GRV-----GRV-- 668
 Qy :|:||:|:||:|:
 Db 715 WTDRAAETAQGLIVY--DYLILKLSVDSVTVSADGTRALVEATLESACUSLSDLVH---- 767
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
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 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
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 ; SEQUENCE 50, Application US/10793626
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 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
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 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
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 ; FILE REFERENCE: PU3-480US
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 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
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 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; GENERAL INFORMATION:
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 ; GENERAL INFORMATION:
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 ; SEQUENCE 50, Application US/10793626
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 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
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 ; FILE REFERENCE: PU3-480US
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 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
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 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
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 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
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 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PU3-480US
 ; CURRENT APPLICATION NUMBER: US-10/793-626-50
 ; SEQUENCE 50, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RIMAHL SGDTKLJIAAFQS----GEDVHRTA 717
 ; TITLE OF IN

Best Local Similarity 18.9%; Pred. No. 1.3; Matches 141; Conservative 108; Mismatches 248; Indels 251; Gaps 37;

Organism: Artificial Sequence
Feature: OTHER INFORMATION: Description of Artificial Sequence: synthetic
Other Information: amino acid sequence
US-10-793-626-1528

Query Match 2.6%; Score 105.5; DB 6; Length 817;
Best Local Similarity 18.9%; Pred. No. 1.3; Matches 141; Conservative 108; Mismatches 248; Indels 251; Gaps 37;

Query Match 124 DALISRRQILQACETLSNPRSRREYNEGLLDEBEATVITDVPDKVPGALCVLQEGBT 183
Db 180 DPVVGDKEITVIEVLLSPRTKVNPLIGE-----PGV-----GKT 215

Query Match 184 EIVLRVGEALLKERLPKSFQDKVLYMALAFDVSRDAMALDPDFITGYEF--VEBAL 240
Db 216 AIAEGLAQATYNEVEPTEIL-----DRVMSLNGTVAAGTKRGEFEERL 261

Query Match 241 KLIQEE-----GASSLAPDILRAQDETLEITPKVLELIGLPIGDD 282
Db 262 KKVMEEHTQAGNVILFIDELHTLVGAGGAEGALDA--SNIKPALARGELOCIGATTLE 31.9

Query Match 283 Y-----AAKR-----INGLGSYRNIIWVGGGASALVGGLTRE 316
Db 320 YRKNIKEKDAALPERRQFIQVDEPTVDTIELKGRLDORYEARHINISDEAFAAKLSD 379

Query Match 317 KFMNEAFLRMTAEEQVDFVA-----TPSNIIPAESFEVYEA---LALVAQAFIGK 364
Db 380 RYVSDEFLPDKAIDLDBASSKVRLKSHTPSNLKEIQEIKVNEKDAAVHAQEF --- 436

Query Match 365 KPHLQDADKQFQQLQQAKVMAEIIPAMLYDTPNNWE---IDFGI--ERGLCALLIGKV 418
Db 437 -ENAAANLRDKQSKLERQYE-----DARKNEWKAQCGDLTALENTAIFIAG-- 482

Query Match 419 DECRMWIGL-----DSBDSQRNPALIVEFVLENSNRDDNDLPGLKCLLTLTLAGVVF 472
Db 483 -----WTGIPLKINTEFDSLRLN---LEDTHKRVQNDANIAISKAVRABRAGL--- 531

Query Match 473 RFRTDKKKFKLGDY-DDPMVWLSYLERVEVYQGSPLAAATMARIQ-AEHYKASANQAL 530
Db 532 -----KDPKRPGPSFELGPGTGKTELARALAEAMSFGEDDAMIRVDMSEFMRKAYSRL 586

Query Match 531 QKVF-----SRYTDRNAAEPKDV-----QETVFSV-----DPVQNN 562
Db 587 VAPPGVGHDDGGLOTEVKVRKPYSVILFDETEKAHDPVENILLQVLDDGHLTDTKGRT 646

Query Match 563 VGRDGEPGVFLAIVARPSSENFTNDYAIRGVSSESSVDETTIEMSVADMILKEASVKLLA 622
Db 647 V-----DEFNVTIIMTSVNGAQELDQRFEGGSEGS_DYETPKT---MKE----- 692

Query Match 623 GVAIGLISLFSQXFLKSSSSFKDNMVSMESEDVATIGSVRADSEALPRMDARTAENI 682
Db 693 -----LNPSF--RPEFLNRRD-DIYVPHKLQTDDELKIVTM----M 726

Query Match 683 VSKWQKIKSLAQPDPDRIEMLPBLVDGMLKWTDRAE-TAQLGLVYDYLKLISVDSV 741
Db 727 VNKL-----THRSL-----EQNINIVVTDKAKEKIAEGYDPEY----- 760

Query Match 742 TVSADGTRALVEA--TLEESACLSLDLV 766
Db 761 -----GARPLIRAIQKTYEDN--LSELII 781

RESULT 6 S-10-793-626-1528
Sequence 1528 Application US/10793626
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: SP2 PHYLLOCOCCUS EPIDERMIDS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: FU348015
CURRENT FILING DATE: 2004-03-04
PRIORITY APPLICATION NUMBER: US20050555478A1
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1518
TYPE: PRT
LENGTH: 817

RESULT 7 US-10-858-730-30
Sequence 30 Application US/10858730
GENERAL INFORMATION:
APPLICANT: Bailey, Richard B.
APPLICANT: Blomquist, Paul
APPLICANT: Doten, Reed
APPLICANT: Driggers, Edward M.
APPLICANT: Madden, Kevin T.

Db 761 -----GARPLIRAIQKTFEDN-LSELII 781

US-10-467-657-5432
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIORITY FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Streptomyces coelicolor
US-10-858-730-30

Query Match 2.6% Score 104.5; DB 6; Length 627;
Best Local Similarity 19.7%; Pred. No. 1.2; Mismatches 208; Indels 210; Gaps 33;
Matches 124; Conservative 87; MisMatches 208; Matches 124;

Qy 241 KLLQSBGASSLAPDRAQIDETLBTPRVLIGPLQDDYAAKRLNGLSGVNRLW 300
Db 10 KVIEAEGARTPSIAYLDG-CEB-----LVGAP----AKR-QAVTNKNTIYA 53
Qy 301 VGGGASALVGGLTREKEWNEAFLR-----MTAEOVQLFLV-----ATPSNIPAES 346
Db 54 -----AKRLIG---HKFEDKEYDIESMPFEIKAHDINGDAWRAKGELSPQQSAEV 104
Qy 347 FEVYEVALLVAQAFIGKPHLQDAKQFQLQOAKWAMEIPAMLYDPRNNWEIDFGL 406
Db 105 LRKNEA---AEAYLGEK-----VTEAVITVPAFFENDSQRQATDAGR 144
Qy 407 ERGL-CALLJGKVDBCRMWGLDSBDSQVRNPALVEF-----VLENSNRDDNDLPG 457
Db 145 IAGLDVKRINEPPTAAALFGMDKDNDRKIAVTDGGTFDISISIEIANLDGKQFEV 204
Qy 458 LCKLLETWLAGVVF-PRFRDTDKKFKLUG---DYYDPMVLSYLE-----RVEVYQGSP 507
Db 205 LATNDTFLGDEDQQLRDYIIDEFKCQGIDLKQDWNALQRKEAAEAKIELLSGQQ 264
Qy 508 L---AAATAATMARIQAEHYKASAMOALQKVYPSPRTDRNSAEPKDQETVSVSDPVGNNVG 564
Db 265 TEINLPYITMDATPKHL---AMKITRAKESLVED-----TVEMSYADMLK 613
Qy 565 RDGEPGVFIAEAVRPSENFTNDYR-AGVSESSVDET-----
Db 298 -----LIARSIEPCT-----ALKDAGLSTGDIDDYLVGGOSRMPKVQEAVYDFFG 344
Qy 614 EASYK-----ILAAAGVAGLISLFSQKYFLKSSSSFQRKDM---VSSMESDVATIGSV 663
Db 345 KEPRKDVNPDDEAVVGAAT-----QGEVLSGG--RSVDLILIDVTPLSLGIETMGGV 393
Qy 664 RADDSALPRMDARTAEN-IVSKWQIKSLAFGPDPDHLEMPLBYTDGRMLKIWTRAAE 721
Db 394 -----MTKLIQQTNTTPIKASQVSTA-EDNQSAVTHVLOGE---RERASA 436
Qy 722 TAOLG-----LIVYDT-----LILKLSV-----DSVTVSADGTRAL---751
Db 437 NKSUQOFNQDIAPARPMQIETFIDANGLHSKDKGTAANITIQGSSLSEE 496
Qy 752 -----VEATLEESACISLIVHPEMNA 772
Db 497 EIERMVQDAEANAEEDKCLTLEYASRNQA 525

RESULT 8
US-10-467-657-5432
; Sequence 5432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 70
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

RESULT 9
US-10-467-657-70
; Sequence 70, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 70
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-6322

Query Match 2.5%; Score 103.5; DB 6; Length 2004;

Best Local Similarity 19.6%; Pred. No. 7.8; Mismatches 209; Gaps 36;

Matches 145; Conservative 108; MisMatches 279; Indels 209; Gaps 36;

Qy 144 RSRREYNE-----GILDDDEBATVITDVPMDKVSALCVLQBG--GETEVLRV 189

Db 712 KALRHEAESIKRLLAESSIGGLAERVDAVSETAPDKAQMLLSORVEGMFDGRTGKITLV 771

Qy 190 GEALIKERLPLKSFKQDVVLYMALAPLDSRDAALDPDFITGYBFVEEALK-----241

Db 772 AENLTPER-----GPAKTYREELERADGNGLJ 814

Qy 815 RRTADAVQREGTGDAASVRPAVEAAEL-----YAAQRTGGWAG 858

Db 242 ---LLOE---EGASSLAPLRL-AQIDETILEETPRYVLELLGLPLGDDYAAKRNLNGLSG 293

Qy 294 VRNLIW-SVGG-----GASALVGGLTR---EXPMNEAFLRMTAAEQDLFVATPSNIP 343

Db 772 AENLTPER-----AWWAHHELGHRGAAD-----GPAXYREEBLERADGNGLJ 814

Qy 859 IENRYGVKVGNGLKGIAVGLARIAGLRRVLORLAGKAGAMSADVFAMLDLHGNGVE 918

Db 815 RRIADAVQEGREGTCDAASVRPAVEEAEL-----YAAQRTGGWAG 858

Qy 919 GARDAPWGNNHRAIMFARADGAERSKSESKLERRAETIRISGREYPEGGNLREYKRN 978

Db 294 VRNLIW-SVGG-----GASALVGGLTR---EXPMNEAFLRMTAAEQDLFVATPSNIP 343

Qy 400 WEIDFGLERGLCALLIGKVDBCRNLWGL-----DSESDQY-RNPATIWFVLENS-- 447

Db 859 IENRYGVKVGNGLKGIAVGLARIAGLRRVLORLAGKAGAMSADVFAMLDLHGNGVE 918

Db 979 -ALEYG--KSLRGPYVNNDTGRETSISLGRSGSITELRHDKDAFHLSQTAIIPOLIENAVY 1035

Qy 448 ---NRD---DNDDLPGLCKLLETWLAGVVF-----PRFRDTKDKKKFK 483

Db 919 GARDAPWGNNHRAIMFARADGAERSKSESKLERRAETIRISGREYPEGGNLREYKRN 978

Qy 1036 IDTLPNEDLAKNGNDIQG---YEYVGSQINVGADYTVRAAVASRNENRYTDHKLTKE 1091

Qy 484 LGDYDDPMVLSYLERYEVV---QGSPL-----AAAATMARIAGAEHKV 523

Db 909 979 -ALEYG--KSLRGPYVNNDTGRETSISLGRSGSITELRHDKDAFHLSQTAIIPOLIENAVY 1035

Db 1092 KGN-----LSSLUDRVSTTGAESKSPLSGIDDKRKLQIQLQDGKGGIADFDTSAVR 1145

Qy 524 ---ASANOALQKVFPSSYTDNSAEPKDQVETVFSVDPVGNNVRGEPEGVF--IAEV 577

Db 1146 FSAANTIAAIGRTGKKSDLNALKORWDASKGIOLQFLGRQQIEDIYGVLDGLKEYG 1205

Qy 578 RPSENFTNDYATRAGYSESSYDTEVVSMVADMILKEASVKTLLAAGVAIGLISLFSQKYF 637

Db 1092 KGN-----LSSLUDRVSTTGAESKSPLSGIDDKRLLQIQLQDGKGGIADFDTSAVR 1145

Qy 638 LK-SSSSFORKD-----MVSMSMESDVATIGS--VRADDSEALPMDAR 677

Db 1092 KGN-----LSSLUDRVSTTGAESKSPLSGIDDKRLLQIQLQDGKGGIADFDTSAVR 1145

Db 1250 AKYDADPLMRKDAQKRLDGIIRTADGKTEKAEEAVASAGARIARADAATNKAQRAAD 1309

Qy 678 TAENIVSKWOKISSLAFGPDHJTEMPLPVLDGRMLKI-WTDEAETTAQOLGLVYDYLTKL 736

Db 1310 KAAYALEQA-----KHGRETTIADDEADKRLRRLFYADSEAKRA-----IRRA 1352

Qy 737 SVDSVTVS--ADGTRALVEA 754

Db 1353 GADVAAESRACKTDAVRMLEQA 1373

RESULT 12

US-10-467-657-6322 ; Sequence 6322, Application US/10467657

; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA

; APPLICANT: PIZZA Maria Grazia

; APPLICANT: MAGNANI Vega

; APPLICANT: MONACI Elisabetta

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218

; SOFTWARE: Seqin99, version 1.04

; SEQ ID NO: 6322

; LENGTH: 2004

; TYPE: PRT

; ORGANISM: Neisseria gonorrhoeae

RESULT 13

US-11-074-176-98 ; Sequence 98, Application US/11074176

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAuliffe, Olivia

; APPLICANT: Peril, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Therefor

; FILE REFERENCE: 5051-694

; CURRENT APPLICATION NUMBER: US/11/074,176

CURRENT FILING DATE: 2005-03-07
; PRIORITY APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 98
; LENGTH: 565
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
; US-11-074-176-98

Query Match 2.5%; Score 103; DB 7; Length 565;
Best Local Similarity 22.2%; Prod. No. 1.2;
Matches 112; Conservative 67; Mismatches 158; Gaps 30;

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Qy 200 KSFQKDDVLYMNAFLDPDF--ITGYEFVEREALKLQEGEGLSLAPLRA 257
Db 123 KSYQK---MPLALYQIQTFRDENPRPFLGRLRGEFV----MLDGTSFAA-TRE 168
Qy 258 QIDETLEIRITPRYVLELGLPIGGDDYAAKRNLNGSG--VRNILWSVGCGG-----AS 307
Db 169 QDQQFDQDKSAY----KRFKRAGTIVHPVIADSGTMGERNSTEFQAP 213
Qy 308 ALVGG---LTEREKFMNEAFLRMTAAEVDLIF----VATPS-NPAESPEVYE 351
Db 214 RAIGEDTIAATNEKGTYAANLEM-AKSDTQEQPBEAKELTKVATPACDTIKKLAEFLD 271
Qy 352 YALAYVQAFI---GRCKPHILODAKQFOOLQOAKVM-ABEI PAMLYDTNNWEIDFGL 406
Db 272 VPATRIVSKILYADDOKVVLIRGDQINETPKLGHYLDADDIHEA-NTBDLKEIT-GS 328
Qy 407 ERGLCALLIGKV----DEC----RMWLGLDSESDSQYRN-----AIVEFV-L 444
Db 329 EKG---GVGPVNADWADKIADETIVKTLAGVVFPRFRDTDKKKPQGDDYDPPMVDSYLER--- 499
Qy 445 ENSNRDDNDLDPGL-CKLLETWLAGVVFPRFRDTDKKKPQGDDYDPPMVDSYLER--- 499
Db 385 RTANEGBPDVHDLPKFTTSLIEVGH-----PKLGYTTKTMGADFLDONGKA 433
Qy 500 YEVVOQSPPLAAATMARIQAHVKASAMOALQKFVPSRYTRNSAEPKDQYQETVFSYDPMV 559
Db 434 QPVIMG3-----YIGVTRM-----LSAVVEOHDLTRGVAWPEKI-APFEIHIV 476
Qy 560 GNNVRGDRGEQFYIAEVRP-SENFT--MDYAIRAGVS----- 595
Db 477 QMKKNDQ--TELAEKLEKICKSEKVDLYDDRKERAVGKPADADLVGAPPRTITGKAA 534
Qy 596 -----BSSVDPPTVENSVADNLK 613
Db 535 DGIVEVKRPTDEKAVENSIDELDK 558

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RESULT 14
US-10-858-730-27
; Sequence 27, Application US/10858730
; Publication No. US2005255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua J.
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorges, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000

Query Match 2.5%; Score 101; DB 6; Length 711;
Best Local Similarity 19.2%; Prod. No. 2.4;
Matches 138; Conservative 98; Mismatches 244; Gaps 35;

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Qy 169 KVPGALCVLQEGETE--IVLRGEALKLKERLPSFKQDVVLYMALAFDVSRA MALD 225
Db 77 KIYGFF-PKREGKSEKEBILTSLIDRPLPEGFHDIQIVAMVYSDPEIDS--D 132
Qy 226 PPDPFITGYEFVVEALKLQEEGASSLAPLRAQIDETLEEITPRYVLELGLPLGD DYAA 285

```

PRIOR FILING DATE: 2003-05-30
; PRIORITY APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
; US-10-858-730-27

Query Match 2.5%; Score 101; DB 6; Length 403;
Best Local Similarity 21.3%; Prod. No. 0.99;
Matches 76; Conservative 51; Mismatches 109; Indels 120; Gaps 16;

```

Qy 56 SSSSSFATATTATLVSLLPPSITDRPER----HVPPIPDPFGQVLAQGOTHFLTDGIRRA 108
Db 62 SAKAEAFADITNTVVARLIEGYDSSDGFQDGATGVNIGI----GAQSPDQIQVDTA 115
Qy 109 FEARV-----SKPPQFGFSSDALISRQQLQAOACETLSNPRSRREYNEGLD 155
Db 116 HEARVEGAADPLDQSQGACDQGLMFYA----INATPEIMPLPALAHRLSRR----- 163
Qy 156 DEBATVITDVPDKVPGALCVLQEEGETEBIVLRGEALKLKERLPSFKQDVVLYMALAFL 215
Db 164 -----LTEV--RKNGVLPYLPRDGKTOVTI----AYEDNPVPLDVTVISTQHADI 209
Qy 216 DVSRDAMALDPPDPFITGYEFVVEALKLQEEGASSLAPLRAQIDETLEEITPRYVLE-- 273
Db 210 DLEK---TLDPD-----IREKVINTVLDL--AHEILDASTVRVLVNPT 248
Qy 274 ---LGLPLGDDYAAKRNLNGLSGVNL-----WSVGGGA----- 306
Db 249 GKFKVLGGMGD-----AGLTKRKIVTDYGGWARGGAFGSKDPSKVKDRSAYAMRN 301
Qy 307 --SALVGLLTREKFPMNEAFLRMTAAEVDLFVAT-----PSNIPAESFEVYBV 352
Db 302 VAKNVIAAGLAAERVEVQVAY-AIGKAAPVGLFVETFGETETDPVKIBKAIGEVDL 356

```

RESULT 15
US-10-467-657-2966
; Sequence 2966, Application US/10467657
; Publication No. US2005026058A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA, Maria Rita
; APPLICANT: PIZZAI, Mariagrazia
; APPLICANT: MASIGNANI, Vega
; APPLICANT: MONACI, Elisabetta
; TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEAR ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SEQ ID NO: 2966
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
; US-10-467-657-2966

Query Match 2.5%; Score 101; DB 6; Length 711;
Best Local Similarity 19.2%; Prod. No. 2.4;
Matches 138; Conservative 98; Mismatches 244; Gaps 35;

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Qy 169 KVPGALCVLQEGETE--IVLRGEALKLKERLPSFKQDVVLYMALAFDVSRA MALD 225
Db 77 KIYGFF-PKREGKSEKEBILTSLIDRPLPEGFHDIQIVAMVYSDPEIDS--D 132
Qy 226 PPDPFITGYEFVVEALKLQEEGASSLAPLRAQIDETLEEITPRYVLELGLPLGD DYAA 285

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Search completed: December 4, 2005, 12:42:48
Job time : 15 secs

(FILE 'HOME' ENTERED AT 14:25:11 ON 04 APR 2007)

FILE 'BIOSIS, CAPLUS, CABA, AGRICOLA' ENTERED AT 14:25:30 ON 04 APR 2007

L1 47 S FTN2 OR ARC6
L2 22 DUPLICATE REMOVE L1 (25 DUPLICATES REMOVED)
L3 375 S PLASTID DIVISION
L4 39 S L3 AND REVIEW
L5 31 S L4 AND ENGLISH/LA
L6 28 DUPLICATE REMOVE L5 (3 DUPLICATES REMOVED)

REFERENCE/DOCKET NUMBER: MRI/NREL IR# 92-48CON
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303-231-1000
 TELEFAX: 303-231-1098

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2089 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HOMOPOLYMER: NO
 ANTI-SENSE: NO
 US-08-418-893D-23

Query Match Score 143; DB 1; Length 2089;
 Best Local Similarity 20.0%; Pred. No. 0.0096;
 Matches 113; Mismatches 289; Indels 272; Gaps 44;

Query 73 LPPSIDPERHPVPIPDYQVLGAQTFLDGIRRABARVSKPP-----QFGPSDDAL 126
 Db 197 LPNALDK-----LGIFKFIGPTGPVMGSGFEGPDDGP 250

Query 127 ISRQIILQAACETLNSNRSRRYYNEGLID-DEBAYITDVPDKVAGLCVHQEGG---181
 Db 251 LQ-----ADLTGGTIPMELPNKGIVTSADBAVIVANKIGWE-N-GIMIKASEGGGK 301

Query 182 -----ETEIVLR-----VEALLKLERUPKPSFKODPVVWMLAFLDVSDRAMALDP 226
 Db 302 GIRFDVNEADLNFNAFYQVSNEYTGSPIFLMQLCKNASHIEQVQVG----DOHENAVALNG 357

Query 227 PDEITGVEFVEALKLQEGGASSLADPLRAQIDETLEBITPRYVLELLGLPGDDYAK 286
 Db 358 RUCSTQRPF-----OKFEEEGPPSIV-----KETPHM-----ELAAQ 391

Query 287 RLNGLSGRVRNTILWGGCGASALVGLLTREKFMNEAFRLRMTAEQVDLFVA--TPSNIP 343
 Db 392 RL-----TQNIGYQ-GAGTVELYNADNKF-----FILENPLQVHRPVTEGITGANLP 441

Query 344 AES-----FEVYEVALLVAQPTGKPHLQDADKOFQQLQAKVMAEIPA---391
 Db 442 ATOLQVAMGIPLNIPDIRRLYGREDAGYGTDP-----IDFLQERYREL-DSHVIAARITAENP 498

Query 392 -----MLYDTRNNW-EIGFGLERGLCALLIGKVDECRMWLGLDSEDSQY--434

Query 499 DEGFKPSTGSSTERIKPQSTPNWGYFSVGANGGI-----HEFADSQFGH 542

Db 601 -----RNP-----AIVEFLVLENNSNRD-NDDLFGLCQKILE-----WLAGVVF 472

Query 543 LFARKPQEQRQAKVALAKEMVRGDIIRNSVEYLVQKULETEAFKNTIDTSWLDII--600

Query 530 -----LQVVFPSRTYDRAESAPKDVQET-----552

RESULT 2

US-08-418-893D-23

Sequence 23, Application US/08418893D
 Patent No. 5559220

GENERAL INFORMATION:

APPLICANT: ROSSLER, PAUL G
 CITY: OHIOLOGE, JOHN B
 TITLE OF INVENTION: GENE THAT ENCODES ACETYL-COENZYME A
 TITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CRYPTICA
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY
 STREET: 1617 Cole Blvd.
 CITY: Golden
 STATE: CO
 ZIP: 80401-3393

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,893D
 FILING DATE: April 7, 1995
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/104,938
 FILING DATE: September 14, 1993
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: O'CONNOR, EDNA
 REGISTRATION NUMBER: 29,252

Query 598 SYDDETTVEMSVADMILKRAVKVILLAAGYAIGLISLFSQKYFLKSSSFORKDMYSSME-SD 656
 Db 601 -----QPYVEAMKMI-MPIKATESG-----KTHNLNSAGSVSAGDLLASLLELD 806

Query 657 VATIGSY-----RADDSREALPRMDARTA-ENVSKWQKIKSLAFGPDRRIEMPEVLDGR 710
 Db 607 PSRVKKETFSKLDIMESKVDEPQCAVMNTS-----GFNLID-----PEAVAQQ 852

Query 711 MLKIWTWDRAAETAQQLGLVYD-YTLLKLSDVSDSVTSAQDTRALVEATLESACLSLVLHPE 769

RESULT 3

US-08-410-893D-24

Sequence 24, Application US/08418893D

Patent No. 5553220

GENERAL INFORMATION:

APPLICANT: ROESSLER, PAUL G

APPLICANT: OHLROGGE, JOHN B

TITLE OF INVENTION: CARBOXYLASE FROM CYCLOTELLA CRYPTICA

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: NATIONAL RENEWABLE ENERGY LABORATORY

STREET: 1617 Cole Blvd.

CITY: Golden

STATE: CO

COUNTRY: USA

ZIP: 80401-3393

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/418,893D

FILING DATE: April 7, 1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/104,938

FILING DATE: September 14, 1993

REFERENCE/DOCKET NUMBER: MRI/NREL IR# 92-48CON

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: O'CONNOR, EDNA

REGISTRATION NUMBER: 29,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: 303-231-1000

TELEFAX: 303-231-1098

TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 2089 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

US-08-410-893D-24

Query Match Score 143; DB 1; Length 2089;

Best Local Similarity 20.0%; Preq. No. 0.0006;

Matches 169; Conservative 113; Mismatches 289; Indels 272; Gaps 44;

Query 73 LPPSIDRPERHRYPIPIDFYQVLGAQTHPLTGTIRRPEARYSKPP-----QFGFSDDAL 126

Db 197 LPNALIKR-----LGKFKIGFTGPNVSLGKIAANILAQTAKVPSIPWSSSGFPDDGP 250

Query 127 ISRQLIQQAACTLSNPRSRREYNEGILL-----DEATVITDWDKVPGALCYLQEGG-----181

Db 251 IQ-----ADLTERTGTTIMEIFNGKLVTSADEAVTANKTGWN-----GIMMKASEBGGKK 301

Query 182 -----ETEIVL-----VGEALLKERLPKSFQDQDVYUVMALAFDTSRDAMALDP 226

Db 302 GIRFDVNEADLRNAFYQVSNEVIGSPIFMLQCKNRHARIEQIVG-----DQHGNVALNG 357

Qy 227 PDFITGYEFVEEALKLQSEGASSLAPEDLRAQIDETLEETPRXYELLLGLPLGDDYAAK 286

Db 358 RDCSQRFF-----QK1FBGPSPS1P-----KTFHEN-----391

Qy 287 RINGISGVNLILWSVGGASALVCGGLTREKPMNEAFLMTAAEQVDFYA-----TFSNIP 343

Db 392 RL-----TONIGYQ-----GAGTVELYNAADNKFF-----FLENPRLOVEHPTEGIGANLP 441

Qy 344 AES -----FEYEVAVLAQAFIGRKPHLQDADFOOQLQKQWYNAMEPA-----391

Db 442 ATOLQVAMGIPLENIPDIRRLYGRDADYGTD-----IDFLQERYRELDSHYAARTAENP 498

Qy 392 -----MLYDTRNNW-B1DFGLERGLCALLIGKVDECRMVLGUDSEDSQY-----434

Db 499 DEGPKPITSIESIRKQFQSTPNVWYFYSVANGGI-----HEFADSQFGH 542

Qy 435 ---RNP-----AIVEFVLENSRND-NDDLPGLCKLET-----WLAGVVFP 472

Db 543 LFARGPNRREQARKALVAKMEVRGDLTENSVEYLKLULETEAPKNTIDTSWLDDII-----600

Qy 473 RFRTDKRFLGYYDDPNVSLYERVWQGSPLAAATMARIQAEHTKASANQA-----529

Db 601 -----KERSVKV-----EMPSHL-----VVGGAFAVKAFENHVTKATEEKESFRKGQVS 644

Qy 530 -----LQKVFPSRTDRNSAEPKDQET-----552

Db 645 TAGIPGINSFNIEVAYLDTKYPFHVERISPDVYFTLDTNTIDEVTOAEGALLATFGG 704

Qy 553 ---VSVD-PVGENVNDRG-----PGVPIAAEVRS-----ENFETNDYAIRGVSES 597

Db 705 ETRHFGMDPELGLURLSDGATVLMPTFDPSELRTDVTGKVYVRLQDNGATVEAG-----760

Qy 598 SVDETTVNSVADMKEASVKILLAGVAIGLISFSQKFPLKSSESSFQRKDVMSEBE-SD 656

Db 761 ---QPYVETEAMKMI-MPIKATESG-----KITHNLSASGSV1SGDILLASLELKD 806

Qy 657 VATIGSV-----RADDSERLPRMDARTA-ENIVSKWQKIKSLAFGPDRHIELMPEVLDGR 710

Db 807 PSRVTKKIEFTSGKLIDMEKSVKVDLIEPQRAYMVLS-----GFNL-----PVAQQ 852

Qy 711 MLKIWTWDRAAETAQOLGTYD-YTLLKSYDSVTVTSADGTRALVETALBESACKSLDVLHPE 769

Db 853 AIDSATDSSAAAIDLVQVLFEPYRVEQFDGV-TADDVYRTLTKANTE-----TLDVISE 907

Qy 770 NNA 772

Db 908 NLA 910

RESULT 4

US-09-057-969-2

Sequence 2, Application US/09057969

Patent No. 6013451

GENERAL INFORMATION:

APPLICANT: TAN, VICTOR THI WONG

APPLICANT: PHANG, SENG MENG

APPLICANT: TAN, TIEN CHYE

TITLE OF INVENTION: BACILLUS STEAROTHERMOPHILUS DNA

TITLE OF INVENTION: POLYMERASE I (KLENOW) CLONES INCLUDING THOSE REDUCED TO

TITLE OF INVENTION: 3'-TO-5' EXONUCLEASE ACTIVITY

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSSEE: FORMMER LAWRENCE & HAUG LLP

STREET: 745 FIFTH AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10151

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/057,969
 PILING DATE: 09-APR-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KOWALSKI, THOMAS J.
 REGISTRATION NUMBER: 32,147
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 212-588-0500
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 954 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: amino acid

RESULT 5
 US-08-680-326-35
 Sequence 35, Application US/08680326
 ;
 ; Patent No. 5955733
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSE, TIMOTHY M.
 ; APPLICANT: BOSCH, MARTIN X.
 ; APPLICANT: STRAND, KURT
 ; APPLICANT: TODARO, GEORGE J.
 ; TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES
 ; TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL
 ; NUMBER OF SEQUENCES: 152
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1018
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/680,326
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schiff, J. Michael
 ; REGISTRATION NUMBER: 40,253
 ; REFERENCE/DOCKET NUMBER: 29938-20001.00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 813-5600
 ; TELEFAX: (415) 494-0792
 ; TELEX: 706141
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1194 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-680-326-35

Query Match Score 139.5; DB 2; Length 954;
 Best Local Similarity 22.0%; Pred. No. 0.00054;
 Matches 175; Conservative 132; Nismatches 315; Indels 173; Gaps 44;

Y 99 HFLTQIRRAFEARYSKPPQFGSDDALISRRQLOAACETLNSPRSRRY-NEGILDDDE 157
 b 183 HYEADDIGTMAAAREB--GFAVKVKSQRDLTQ---LASPVTVETRKKGTDIE 234

Y 158 EATVITDV-----PMKVPG-----ALCVQEGGETEVTRVG 190
 b 235 SYTPTEVVERKGLTPEQIVDVLGMDKSNONIPGVIGKCTAVKLKQKFCTVENYLASI 294

Y 191 BALLKERLPGFSKQ -DVVIVMALLAFDVSREDA--MALDPDPDFGTGYEVPEALKLQE 245
 b 295 DEIKERKLENLRQYRDAL-LSKQLANIDTADPVELTD-DIVYKGERKRVVALFQE 351

Y 246 EGASSLAPDILRAQIDE-----TLEBRITPRVYLETLGL--PLGDDYAAKRLNG- 290
 b 352 LGFQSFLDKNQVOTDGEKPIAGMDFIAIDSVTDEMELADKAALVVVGDNYHHAPIVG 411

Y 291 LSGCURNILW---SVGGGCGASALVGGLTREKFM-----NEAFDRMTAREQV- 333
 b 412 ALANERGRFFLPRPETAVADDPKFLANGDEPKKTMEDSKRCAAVALNGKGIELAGYGVVF 471

Y 334 LFVATESNIPAES-----FVVYEVALLVAQAFIGK-KPHLLQDADKOFQOL--QOAQ 383
 b 472 LLLAAYLLDQAAGDVAAVARMHOYEAVSDEAVYKGKAGRTPDPTLAEQLYRAAA 531

Y 384 VMAMEI PAMLYDTRNNWE-DIFGLERGLCLLIG----KVDECRM-WLGLD-SEDSQY 434
 b 532 IWALEEPPLMDELRRNNEQDRLLTEHALAGLANNMEFTGKVDTKLEQMGAEITELQQL- 590

Y 435 RNPATFVJENSNRNDIDPGLCKLLETLAGVIFPRFDTDKFKFLDDYDDPPMV 494
 b 591 --AVERRTELAGQEFNISP--KQLGT--VLFDKLQLPVLKKTKG-YSTSADV 639

Y 495 SYL-ERVEVYCGSPAAAATMARIAGHEHVAKASAMOQKYPFSRYSRDNSAEPKVQET- 552
 b 640 EKLAPHEIV--HILHYRGQKLGOSTYE-GLLKVKVHPYPTGKVHMENQ---LTTQG 692

Y 553 -VFSVDPGVNVRGDCGPFGFIAEVAPSE-----NFTENDYAIRGAYSESSYDET 603
 b 693 RLSSYEPNLQNPILIPRLEEGRKIRQAFVPSPDWLPAADYSQIELRVLATAE---DDNL 749

Y 604 VE-----MSVADLKE--ASVCKLAAGVAGIQLSLFSOKYFURSSSFQRK 647
 b 750 IEAFPRWLDLHTKTMANDIHFVSEEDVTANMRQAKAVNFGIVYGISD-YGLAQNLNITRK 808

Y 648 DMVSSMSESDYATIGSYRADDSPEALPRMDARTAENTVSKWOKIKSLAFGPDRHIEMLPEVL 707
 b 809 EAAEFTERYFAFPFGTK-----QMDNIIQ-EAKQGYTTLHRRYLPDIT 855

Qy 176 VL---QEGGETBIVLRYGEAIIKERLPSKFQK-----DVVLVMLAFLDVRSR 220
 Db 205 NDATLNGDKNAFQTGTSKPSASPEPSREV--IERTDYYQDQPCAPYVSPSKFTN 261
 Qy 100 FLTDGIR---RAPEARRYSKPPQGFSDDALIS-----RQI----- 132
 Db 262 YLCDFNFHBLKYYGRVDAATRFLMDNPFGFWQLKPGVGDGERVVRPASRQTLSD 321
 Qy 133 LQAC-----ETLSPNRSRREYNEGILDE-----BATVITDVPWDKPGALC 175
 Db 322 VETCDMSDNQLAIPNDDSWPDYKLLCFDIECKSGGSNELAFTPATHLED-----VIQISC 377
 Qy 176 VL---QEGGETBIVLRYGEAIIKERLPSKFQK-----DVVLVMLAFLDVRSR 220
 Db 378 ULYSTPSPROSILENTTSFSGSCDIPORTYVORMKDAGI, PRPTVIL, RFDSEPPULIAATPLVVK 437

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/394,232
 FILING DATE: 08/307,410
 APPLICATION NUMBER: 08/394,194
 FILING DATE: 16-SEP-1994
 APPLICATION NUMBER: 08/222,612
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: GP94003.CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-3807
 TELEFAX: 619-546-7929
 TELEX:

SEQUENCE FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 876 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US -08-436-664-20

Query Match Score 128 5; DB 1; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 135; Mismatches 302; Indels 201; Gaps 43;

Qy 99 HPLTDGIRRAFEARVSKEPPQFGSDDALISRQQLQAACTLSNPRSRREY-NEGILDDE 157
 Db 107 HYEADDIGITMARAERE--GFAVKVISGRDRDUO---LASPTQVTEBTKKGITDIE 158
 Qy 158 EATVITDV ----- PWDKVPGP --- ALCQLQEGGETETVLTRVG 190
 Db 159 SYTPETTIVVKYGLTPEQIVDLKGLMDKSNDNIPGYPGIGEKTAVKLKGQTGVENTLASI 218
 Qy 191 EALKERLPKSFQO-DVYLVMALAFLDYSRDA---MALDPPDFITGYFVEEALKLQE 245
 Db 219 DEIKGEKLENLRQYRDL-LSKQLAICRDAPVLTID-DIVYKGDERKVAFQFQE 275
 Qy 246 EGASSLAPPDLRAQIDE ----- TLEETITPRYVLELLGL---PLGDDYAAKRLNG- 290
 Db 276 LGFQSFLDKMAYQDGEKPKLAMDEAFLDPSVTDEMALKAAALVVEVVGDNYHAPIVG1 335
 Qy 291 ----- LSCTVRNTIWSVGGGASALVGGLTREKPMNAFLRMTAAE----- KPHLLQ 370
 Db 336 ALANERGRFLRPLADPKFLW----- LGDETJKKTMDRSRAAVALKWKG1 385
 Qy 331 ----- QDILFLVATPSNIPAES----- PEVVEVALVAQAFIK----- KPHLLQ 330
 Db 386 ELRGVVFIDLAAYLDPQAAGDVAVAKMHQYEAVRSDEAVYKGAKRTVPDEPLAE 445
 Qy 371 DADKQFOQLOQAKTMAEIPAMLYDTRNWE-IDFGLERGLCALLIG----- KYDECIM 423
 Db 446 HLAR ----- KARAIWALBEPLMDELRNEDQRLTLEPLAGLIAANMEFTGVKVTKRL 500
 Qy 424 -WLGLD-SEDSOQRNPALIVEFLNSRNRDDNLPLGCKLLETWLGIVFPRFRKDCK 481
 Db 501 EONGAELTBQLQ --- AVERRIVELAGQFNINSP----- KOLGT --- VLFDKLQLPVLK 549
 Qy 482 PKLGDDYDDPMVLSYL-ERVEVQGSPPLAAATMARIGAEHKVASAMQALQKFPSRYTD 540
 Db 550 TKTG-YSTSADVLEKLAPHEIYB-HHLHYROLGKLOSTYE-GLLKIVHHPVTCVKVHTM 605
 Qy 561 RNAEAPDQVET-VFSYDPMGNVGRDGEPGVFAEAVRPSE----- NFETNDYAI 590
 Db 606 FNOA---LTQTRGRLSSVEPNLQNIPRLEEGRKIRQAOFVPSEDDWLIFADYSOIELRV 661
 Qy 591 RACVSESSVDETTE----- MSVADM1KE --- ASVILLAAGVAIGLISLFSQ 634

RESULT 6
 US-08-436-664-20
 Sequence 20, Application US/08436664
 Patent No. 5674282
 GENERAL INFORMATION:
 APPLICANT: RIGGS, MICHAEL G.
 APPLICANT: SIVARAM, MATROOR
 APPLICANT: TUDOR, STARLA D.
 TITLE OF INVENTION: STEAROTHERMOPHILUS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gen-Probe Incorporated
 STREET: 9880 Campus Point Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disquette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSBQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,664
 FILING DATE: 08-MAY-1995
 CLASSIFICATION: 536

RESULT 7
US-08-436-664-32
; Sequence 32, Application US/08436664
; Patent No. 5874282
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Discrete
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436, 664
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394, 232
; FILING DATE:
; APPLICATION NUMBER: 08/307, 410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222, 612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-436-664-32

Query Match Score 128.5; DB 1; Length 876;
Best Local Similarity 21.0%; Pred. No. 0.0056;

Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;
Qy 99 HFLTDGTRAFEARVSKEPQFGSSDDALISRRQILQAACTLSNPRSRREY-NEGLLDDE 157
Db 107 HYEADDLIGTMARAERE--GFPAVKVSGDRDLTQ---LASPOVTVEITKGKIDIE 158
Qy 158 EAFTVITY------PMDKYPG-----ALCVLQEGGETBIVLRYVG 190
Db 159 SYTPETTEVKYGLTPQEVLVDLGKMGDKSDNIFGVPIGEKTAVKLQKFGTVNLASI 218
Qy 191 EALKERLPKSFQ -PYVLYMVALAFLDVRSRDA--MALDPPDFITGYBFVEEALKLQE 245
Db 219 DEIKGEKLKENLQRYRDIAL-LSKQLAACRDAPEVLTLD-DIVYKEDREKVHALFQE 275
Qy 246 EGASSLAPPDLRAGDE-----TLEETTPRVYELIGL--PGSDYAAKRLNG- 290
Db 276 LGFQSFPLDKMAYQTGEGEKPLAMDFEADSVTDEMILADKAALAVVYEVGDNYTHAPIVGI 335
Qy 291 -----LSGVRNTILWSVGGGASALVGGSLTREKMPNEAFLRMTAAE---- 330
Db 336 ALANERGRFFPLRPLTADPKFLAW-----LGDETKCTMFDSRAAVALKWKGI 385
Qy 331 -----QYDLFVATPSNIPAES-----FEVYEVALLVAQAFIGK-----KPHLJQ 370
Db 386 ELRGVVFPDLLLAYLDPQAAGDVAAYKMHOEYARSDEAYKGAKRTVDPDPBLAE 445
Qy 371 DADKQFQOLQOQAKUMBIAPAMYDITRNWE-LDFGLERGLCALLIG-----KVDCECM 423
Db 446 HLAR-----KAAIAWALEEPLMDELRNQEQDRLLTEQPLAGTLNAMEFTGV/KVDTKRL 500
Qy 424 -WLGLD-SESDSOYRNPAIVEFVLENSNRDDDLPLGICLKLTWTLAGVVFPRFDTKRK 481
Db 501 EONGAELTEQLQ ---AVERRVYELAGQEFNINSP---KQLGT---VLFDKLQLPVLK 549
Qy 482 FKLGDDYDDPMVLSYL-ERVEVYQGSPPLAAATMARIAGAEHYKASAMQALQVPPSRYTD 540
Db 550 TKTG-YSTSADVLEKLAPHEIVE-HHLHYROLKGLOSSTYIB-GLLKVVHPPTGKVHFM 605
Qy 541 RNSAEPDVQET -VFSDVPVGNNVGRDGEPEGYVIAEVRPSE-----NEFTNDYAI 590
Db 606 FNQG-----LTOIGRLSSYEPNLQNIPTRLEEGKIRQAFVPSPDMLIIFAADSQIELRV 661
Qy 691 RAGVSESSVDETTE-----MSVADMILKS---ASTKLLAAGVAIGLJSLSFSQ 634
Db 662 LAHIAE --DDNLJEAFRGLD1HTKTANDIFVSEBDTANMRQAVAVNFGIVYGISD 718
Qy 635 KYFLKSSSSFORKDMVSSMESDVTATGYSVRADSEALPRMDARTAENIVSKWOKIKSLAF 694
Db 719 -YGLAQINNITRKEAEEFERYFASFPGVK-----QYMDNTVQE-AKQGYYT 764
Qy 655 GDPHRIEMLPVIDGRM-LKIWTDRAA-ETAQLGLVVDYTLKLSVD-SVTVSADGTRA- 750
Db 765 TLHRRVYLPDITSRNFNVRSAERTAMNTPIQGSAAD-IIKCAMIDLSVRLSERLQAR 823
Qy 751 -----LYBATLEESACLSDIYHPE 769
Db 824 LLLQVHIDELILEAPEEERLCLLV-PE 850

RESULT 8
US-08-436-664-34
; Sequence 34, Application US/08436664
; Patent No. 5874282
; GENERAL INFORMATION:
; APPLICANT: RIGGS, MICHAEL G.
; APPLICANT: SIVARAM, MATHOOR
; APPLICANT: TUDOR, STARLA D.
; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACTILLUS
; TITLE OF INVENTION: STEAROTHERMOPHILUS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Discrete
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436, 664
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/394, 232
; FILING DATE:
; APPLICATION NUMBER: 08/307, 410
; FILING DATE: 16-SEP-1994
; APPLICATION NUMBER: 08/222, 612
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A
; REGISTRATION NUMBER: 36,510
; REFERENCE DOCKET NUMBER: GP94003.CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLogy: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-436-664-32

CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: PASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,664
 FILING DATE: 08-MAY-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/394,232
 FILING DATE:
 APPLICATION NUMBER: 08/307,410
 FILING DATE: 16-SEP-1994
 APPLICATION NUMBER: 08/222,612
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: GPP94003.CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-2807
 TELEFAX: 619-546-7929
 TELEX:

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
 LENGTH: 876 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE: US-08-436-664-34

Query Match Score 128.5; DB 1; length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

Db 99 RPLTDGIRRAFFARVSKPQPFSSDALLSRQIQLQACETLSNPRTREY-NEGILIDDE 157
 107 HYEADDLIGTMAAARE--GFAVKVTSGRDLTQ---LASPVQTVEFKRGTIDIE 158

Qy 158 EATVITDV-----PWDKVPG-----ALCVLOEGGETEIVLRVG 190

Db 159 SYTPETVKEGLTPEQIVDKLGMGDKSNDNTPGVPIGETPAVKKLKQFGTVENVLASI 218

Qy 191 BALLKEKLPSFKQ--DVIIMALAFDVSRA--MALDDDPDFGYEF/SEALKLKQB 245

Db 219 DEIKGEKELKENURQYDALL-SKSQLAICRDAPVELTLD-DIVYKGDEREKVWALFQE 275

Qy 246 EGASSIAAPDIAQIDE-----TLEETTPRYLELGL---PLGDDOYAARKRLNG- 290

Db 276 LGFQSPLDRMVAQTDTGKPKAGMDFAIDSVDIEMADKAALAVVEVGDNTHHAPIVGI 335

Qy 291 -----LSGVNILMSVGGGASALVGGLTREKEMNEAFLMTAAE--- 330

Db 336 ALANERGRFRRPETALADPFLAW-----LGDETTRKTMDFSKRAAVALKWKG1 385

Qy 331 -----QVDLFTATPSNIPAES-----FETYEVALVALDAF1GK-----KPHLHQ 370

Db 386 ELRGVVFDLIILAYLLDPROAGDVAAVAKHOYEAVSDEAVYGRGAKRTPDDETLAE 445

Qy 371 DADKQFQQLQOAKYNAMEIIPAMLYDTRNNWEIDFGHLERGICALLIG-----KVDECIM 423

Db 446 FLAR----KAAAIWALEEPIPMDLERNEODRLLTLEQPAGILANMBFFGKVKDTRK 500

Qy 424 -WLGLD-SEDSQYRNPAIVEFVLENSNRDDNDLPLGCKLLETWLAGVVFPRFDTKDKK 481
 501 EQMGAELTEQLQ---AVERRIYELAQEFNINSP---KQLG---VLFDKLQLPVLK 549

Db 482 FKLDQYDDEPMVLSYL-ERVEVVOGSSPLAAAATMARIQAEHKASAMOALQKVFPSSRYTD 540
 550 TKTG-YSTSADVLEKAPHBIVE-HILHYROLGLQSTY-EGLKWKHVTGKVHTM 605

Qy 541 RNSAFPKDQVBT-VPSYDPUGNNVGRDGECPVFILEAVRSE-----NFETNDYAI 590

Db 606 FNQA---LTQTCRSLSVENPNQNPIRLEGRK/ROAFVSEPDWLI/FAADYSQEELRV 661

Qy 591 RAGVSESSVDETTV-----MSVADMURK---AVSKILAAQVATGLISLFSQ 634

Db 662 LAHTAE---DDNLTEAFRGLDIHTKTMADI/PVSEEDVTANMRQAKAVNFGIVGJSD 718

Qy 635 KYFLKSSSFORKOMVSSMESDVATISVRAADDSEALPRMDARTAEMIVSKWOKIKSLAF 694

Db 719 -YGLAQNLNTRKEAALETFERYFASFPGV-----QYMNIVQE-AKQGCVYT 764

Qy 695 GDPDIRLEMPEVULGORM-LKIWTBRA-ETAQGLVYDPTLKLSDV-SVTVSADGTRA- 750

Db 765 TLLHRRVYLDTTSRNENVRSFARTMTNPIQGSAAD-TIKKAMMDLSVTREREQLQAR 823

Qy 751 -----LVEATLESACLSLIVHE 769

Db 824 LLLQVHDELLLEAPEKBEIRLCLRV-PE 850

RESULT 9
 US-09-135-642-20
 Sequence 20, Application US/09135642
 ; Patent No. 606683
 ; GENERAL INFORMATION:
 ; APPLICANT: RIGGS, MICHAEL G.
 ; APPLICANT: SIVARAM, MATHOOR
 ; APPLICANT: TUDOR, STARLA D.
 ; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
 ; TITLE OF INVENTION: STEAROTHERMOPHILUS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gen-Probe Incorporated
 ; STREET: 9880 Campus Point Drive
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/135,642
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/394,232
 ; FILING DATE: 08/30/94
 ; APPLICATION NUMBER: 08/307,410
 ; FILING DATE: 16-SEP-1994
 ; APPLICATION NUMBER: 08/222,612
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fisher, Carlos A
 ; REGISTRATION NUMBER: 36,510
 ; REFERENCE DOCKET NUMBER: GPP94003.CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-546-7929
 ; TELFAX: 619-546-7929
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 876 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-09-135-642-20

Query Match Score 128.5; DB 2; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

Qy 99 RFLDGTIRRAFARVSKPQFGSSDDALISRQILOACETLSNPSRSRRE--NEGILIDDE 157
 Db 107 HYEADDLIGTMARAERE--GFAVKVSGDRDLTQ---LASPVQTVETTKKGTDIE 158
 Qy 158 BATVITYDV-----PWDKVPG-----ALCVLQEGGSETETIVLRVG 190
 Db 159 SYPTEPVEKGLTPEQIVDQLKGMLGDKSDNTIPGVPGIGETAVKLKOFSPVENTIASI 218
 Qy 191 EALKERLPKSFQ--DVVLIMALAFDVSRA--MALDPDPDFTYEFTEBAKLLOE 245
 Db 219 DEIKGERKLKENURQYRDLA--LSKLAICRDAPVETLDA--DIVYKGDEKEVVAFLQF 275
 Qy 246 RGAASSLAPDLRAQIDE-----TLEETPTPRYELLGQI---PLGDYDAAKRLNG- 290
 Db 276 LGFQSFDLKRMAVQTDEGEKPLAGMDFAIASYDVTDEMADKAALUVVVGDNTHAPIVGI 335
 Qy 291 -----L-SGVRNJIWLSSVGGGASALVGLLTREKEMNEAFLMTAAE---- 330
 Db 336 ALANERGRFRFPLTAW-----LGDETCKTMFDSKRAVALWKGI 385
 Qy 331 -----QVDLPLPATPSNPAES-----FETYEVALLVAQFQIGK-----KPHLHQ 370
 Db 386 ELRGVYFEDLLAAYLLDPAQAAGDVAAVAKHQQYBAVRSDAEVYGGAKRTVDPDEPLAE 445
 Db 371 DADKQFOOLQKQVNAMEIPAMLYDNTNNW3-IDFGIQLRGLCALLIG-----KVDECRM 423
 Db 446 HLAR----KAAAIWAILEEPMLDELRRNEQDLILTEQPLAGILANMEFTGVKDITKRL 500
 Qy 424 -WLGLD-SESDQYRNPAIVEFYLENSRNRDDNDLPLGQCLKLJLETWLAGVVFPRFRDTKDKK 481
 Db 501 EOMGAELTEEQLO----AVERRIYELAQEFNINSP---KQLG----VLFPLQLPVLK 549
 Qy 482 FKLGDDYDDPMVLSYL-ERVETVYQGSPLAAATMARGAETHYKASAMQALQKVPPSRYTD 540
 Db 550 TKTG-TSTSADVLEKAPHBEE--HILHTRQLGKLUQSTYIE-GLIJKVHPVTKVHTM 605
 Qy 541 RNSAEPKDVOET--VFSTDPVGNVNRGDEPFAVTPAIAVRE-----NFETNDYAI 590
 Db 606 FNOA---LTQGRLLSSYEPNQNP1RPLEGRKIROAFVPSSEPDLIFADYSQELRV 661
 Qy 591 RAGVSESSVDETTE-----MSVADMLKE--ASVYKLAAGVAGLGLISFSQ 634
 Db 662 IAHIAE---DDNLIAEPRGRDLIHTKPTMDITHVSEDTVANMRROAKAVNFGIVGSD 718
 Qy 635 KYFLKSSSSPKQDMVSSMESDVATISYRADDSRALPRMDARTAENIVSKWQKIKSLAF 694
 Db 719 -YGLAQUNLNTKKEAABFIERVYFASPPGVK-----QYMONIVQB-AKORGYVT 764
 Qy 695 GDHDRTIELMPEYLDGRM-LKINTDRAA-ETAQGLYDYDYLKLSPVTSADGTRA- 750
 Db 765 TLLHRRXLPDTSRNPVNRSFAERTAMNTPIQGSAAD-IKKAMIDLSSVRLREERLQAR 823
 Qy 751 -----LVEATLLEESACISLSDLVHP 769
 Db 824 LILQVHDELLIEAPKGEETERLCRLV-PS 850

US-09-135-642-32
 ; Sequence 32, Application US/09135642
 ; Patent No. 606483
 ; GENERAL INFORMATION:
 ; APPLICANT: RIGGS, MICHAEL G.
 ; APPLICANT: SIVARAM, MATHOOR
 ; APPLICANT: TUDOR, STARLA D.
 ; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
 ; TITLE OF INVENTION: STEAROTHERMOPHILUS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gen-Probe Incorporated
 ; STREET: 9880 Campus Point Drive
 ; CITY: San Diego
 ; STATE: CA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/135,642
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/394,232
 ; FILING DATE:
 ; APPLICATION NUMBER: 08/307,410
 ; FILING DATE: 16-SEP-1994
 ; APPLICATION NUMBER: 08/222,612
 ; FILING DATE: 16-SEP-1994
 ; NAME: Fisher, Carlos A.
 ; REGISTRATION NUMBER: 36,510
 ; REFERENCE DOCKET NUMBER: GP94003.CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-535-2807
 ; TELEX: 619-546-7929
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 876 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-09-135-642-32

Query Match Score 128.5; DB 2; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

Qy 99 HFLTDGTRRAFARVSKPQFGSSDDALISRQILOACETLSNPSRSRREY-NEGILDDE 157
 Db 107 HYEADDLIGTMARAERE--GFAVKVSGDRDLTQ---LASPVQTVETTKKGTDIE 158
 Qy 158 EATVITYDV-----PWDKVPG-----ALCVLQEGGSETETIVLRVG 190
 Db 159 SYTPEPYEKYGLPEQIVDLSKUMGDKSDNIPCVPGIGEKTAVKLKQFGTVENVLASI 218
 Qy 191 EALKERLPKSFQ-----LGDETCKTMFDSKRAVALWKGI 385
 Db 219 DEIKGERKLKENURQYRDLA--LSKLAICRDAPVETLDA--DIVYKGDEKEVVAFLQF 275
 Qy 246 EGASSLAPDLRAQIDE-----TLEETPRYVLELLGI---PLGDDYAAKRLNG- 290
 Db 276 LGFQSFDLKRMAVQTDEGEKPLAGMDFAADSVDLMAKPLA 335

FILING DATE: 16-SEP-1994
 APPLICATION NUMBER: 08/222,612
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFILE/DOCKET NUMBER: GP94003.CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-2807
 TELEFAX: 619-546-7929
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 876 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-09-135-642-34

Query Match Score 128.5; DB 2; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

99 HFLTDGIRRAFEARVSKPPQFGFSDALISRROLQAACETLSNPSSREY-NEGILJDE 157
 107 HYEADDIIGITMAAARE--GFAVKVISCDRDTQ---LASPVTVETIKKGITDIE 158

99 HFLTDGIRRAFEARVSKPPQFGFSDALISRROLQAACETLSNPSSREY-NEGILJDE 157
 107 HYEADDIIGITMAAARE--GFAVKVISCDRDTQ---LASPVTVETIKKGITDIE 158

158 EATVTDV-----PDNDKVPG-----ALCVLQEGGETEIVLRVG 190

159 SYTPEVVKEVKGLTPQEIVDLKGLMGDKSDNIPGVPIGIGEKTAVKLIKQFGTENVLASI 218

191 EALLKLRLERKLNRLQYRDL-LSKOLAAICRDAPVLTLD-DIVVKGDEREKVVLQFQE 275

219 DEIKGERLXENLRLQYRDL-LSKOLAAICRDAPVLTLD-DIVVKGDEREKVVLQFQE 275

246 EGASSLAPDLRAQIDE-----TLEBITPRVYLELLGL--PLGDDYAAKELNG- 290

276 LGFQSFIDRMAVQTDEGEKPLAGMDFAIADSVTDEMADRAALVYVEVGDNYHHAPIVGI 335

291 -----LGGVRNIILSVEGGGASALVGGLTREKFNEAFLRMTAAE---- 330

336 ALANERGRFFLRPETAIDPKFLAW-----LGDETKKKTMEDSKRAAVALKWKGI 385

331 -----QVDLFVATPSNIPAES-----PEVVEVALALVAQAFICK-----KPHLHQ 370

386 ELRGCVFDLILAYLDPAQAAGDVAVAKMHQYEAVRSDBAVIGKGAKRTPDEETLAE 445

371 DADKQFOQILOQQAKWAMEI PAMLYDTRNNWE-IDFGLERGLCALLIG-----KVDBCRM 423

446 HLAR-----KAAAATWAEEPLMDLRNEQDRLLTEQPLAGTIANMBEFTGKVTKRL 500

424 -WIGLGLD-SEDSQVRNPAAVEFLVLENNSRDDNDLPGLKQLETLWAGVVPRFRDTKDKE 481

501 EQMGAELTEQLQ---AVERRIYELAGQEFNINSP---KOLGT---VLFDKLQFVLKK 549

482 FKLGDDYDPMVSYL-ERVEVYQGSPLAAATMARIAGHVAQKUFPSPRYD 540

550 TKTG-YTSADSADLEKLAPEHEI VS-HILHYRQGKLQSTYIE-GLKVVHPVTKVHTM 605

541 RNSAEPKVQET-VFSVDPVGNVGRDCEPGVPIAEAVRPE-----NFETNDYAI 590

606 ENQA---LTOTGRLSSTBPNLONIPRILEEGRKIRQAVVPSEPDWLIFADAYSQELRV 661

591 RACVSESSYDETVE-----MSVADMNLKE--ASVKLLAAGVAIGLISLFSQ 634

662 LAHIAE---DDNLIEAFRRGLDINTKTAMDIFVHSEEDVTANMRQAKAVNFGITYGISD 718

635 KPYLKSSSSFRQKDMYSSMESDVATIGSVRADDSALEPRMDARTAENIVSRQOKISLAF 694

719 YGLAQNLNITRKEAEEFIERYFASPFGVK-----QYMDNIVQE-AKOKGYVT 764

695 GDDHREMLPFLDGRN-LKHWTDRAA-ETAQOLGLVYDYLKLISLSDV-SVTVSADGTRA- 750

765 TLLHRRYLPDITSRNENVRSAERTAMNTLQGSAARD-IKKAMIDLSVRLREERLQAR 823

751 -----LYEATLREESACSLDLYHPE 769

824 LLLQVHDELILEAPKEIERLICRLV-PB 850

RESULT 11
 Sequence 34, Application US/09135642
 Parent No. 606483
 GENERAL INFORMATION:
 APPLICANT: BIGGS, MICHAEL G.
 APPLICANT: SIVARAM, MATHOOR
 APPLICANT: TUDOR, STARLA D.
 TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 STREET: 9880 Campus Point Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/135,642
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/394,232
 FILING DATE:
 APPLICATION NUMBER: 08/307,410
 APPLICATION NUMBER: 08/307,410

QY 291 -----LGGVRNIILSVEGGGASALVGGLTREKFNEAFLRMTAAE---- 330
 Db 626 ALANERGRFFLRPETAIDPKFLAW-----LGDETKKKTMEDSKRAAVALKWKGI 385
 QY 331 -----QVDLFVATPSNIPAES-----PEVVEVALALVAQAFICK-----KPHLHQ 370
 Db 765 ELRGCVFDLILAYLDPAQAAGDVAVAKMHQYEAVRSDBAVIGKGAKRTPDEETLAE 445
 QY 371 DADKQFOQILOQQAKWAMEI PAMLYDTRNNWE-IDFGLERGLCALLIG-----KVDBCRM 423
 Db 446 HLAR-----KAAAATWAEEPLMDLRNEQDRLLTEQPLAGTIANMBEFTGKVTKRL 500
 QY 424 -WIGLGLD-SEDSQVRNPAAVEFLVLENNSRDDNDLPGLKQLETLWAGVVPRFRDTKDKE 481
 Db 501 EQMGAELTEQLQ---AVERRIYELAGQEFNINSP---KOLGT---VLFDKLQFVLKK 549
 QY 482 FKLGDDYDPMVSYL-ERVEVYQGSPLAAATMARIAGHVAQKUFPSPRYD 540
 Db 550 TKTG-YTSADSADLEKLAPEHEI VS-HILHYRQGKLQSTYIE-GLKVVHPVTKVHTM 605
 QY 541 RNSAEPKVQET-VFSVDPVGNVGRDCEPGVPIAEAVRPE-----NFETNDYAI 590
 Db 606 ENQA---LTOTGRLSSTBPNLONIPRILEEGRKIRQAVVPSEPDWLIFADAYSQELRV 661
 QY 591 RACVSESSYDETVE-----MSVADMNLKE--ASVKLLAAGVAIGLISLFSQ 634
 Db 662 LAHIAE---DDNLIEAFRRGLDINTKTAMDIFVHSEEDVTANMRQAKAVNFGITYGISD 718
 QY 635 KPYLKSSSSFRQKDMYSSMESDVATIGSVRADDSALEPRMDARTAENIVSRQOKISLAF 694

RESUIT 12
 ; Sequence 20, Application US/08394232A
 ; Patent No. 6100078
 ; GENERAL INFORMATION:
 ; APPLICANT: RIGGS, MICHAEL G.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: SIVARAM, MATHOOR
 ; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILUS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gen-Probe Incorporated
 ; STREET: 9880 Campus Point Drive
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Discrete .. -
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/394,232A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/307,410
 ; FILING DATE: 16-SEP-1994
 ; APPLICATION NUMBER: 08/222,612
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fisher, Carlos A
 ; REFERENCE/DOCKET NUMBER: 36,510
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-515-2807
 ; TELEFAX: 619-546-7929
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 876 amino acids
 ; TYPE: amino acid
 ; STRANDENESS: single
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-394-232A-20

Query Match Score 128.5, DB 2; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

Qy 99 KFLTDGIRRAFPARVSKPQFGTSDDALISRQLQACETISNPRRREY-NEGILIDDE 157
 Db 107 HYEADDLIGTMAARATE--GPAVKVISGRDLTQ---LASPQTIVETTKKGITDIE 158
 Qy 158 BATVITYD-----PWDKVPG-----ALCVLQEQQGETEIVLRVG 190

Db 719 -YGLAQNLNITRKAEAFFEIEFYFASPGVK-----QYMDNIVQ-B-AKQKGYVT 764
 Qy 695 GDPHERTEMLPVLDGRM-LKWTDRSA-ETVQGLVYDYLTLKLSTD-SVTYSAADTRA- 750
 Db 765 TLLHRRYRLPITSRNENVRSAERTAMNTPIQGSAAD-TIKRAMIDLSVRLREERLQAR 823
 Qy 751 -----LVEATLEESACSLDVHPE 769
 Db 824 LLLQVHDELITLEAPCEHEIERLCRLV-PE 850

Db 159 SYTPETVYEVKGYLTPEQIVDLSKLGMSDNIPCPVPGIGEKTAVKLLKGQFGTVNLVLA 218
 Qy 191 EAIILKPERLPKSFFQ-DVVLVMAFLAFVLSRDA--WALDPPDTITGTYFVEEALKLQE 245
 Db 219 DEIKGEUKENDRQYRDIAL-LSKQLAAICRDAPVLTID-DIVYKGEDREKVTLFQE 275
 Qy 246 EGASSLAPDLRQIDE-----TLEETIPRYVLELGL---PLGDDYAAKRLNG- 290
 Db 276 LGFQSFLDKMAYQDGEKPLACMDFAADSVDTEMADKAALYVEVVDNYHIAPIVGI 335
 Qy 291 -----LSGVRNLLWSVGGASALVGGLTREKPMNEAFLRMTAE----- 330
 Db 336 ALANERGRFELRBTALADPKFLAW-----LGDETKKTMFDSKRAAVLKWKGI 385
 Qy 331 -----QVDFLFVATPSNTPA-----FEVYEVALLAQAQAFGK----- 370
 Db 386 ELRGVVFDLILAYLLDPAQAAGDVAAVARMHQTEAVRSDEAVYGKAARTVDPDFTLAE 445
 Qy 371 DADKQFQDQLOQAKVMAEBIPAMLYDTRNNWE-1DFGLERGLCALLIG-----KVEDCRM 423
 Db 446 HILAR-----KAAIAIWALEPLMDBLRQEQRDLITELRQPLAGIANNMEFTGVKVDTKRL 500
 Qy 424 -WLGGLD-SEDSQYRNPAVLFVLENSRNDLPLGCKLLETLMAGV/FPRFRDTDKX 481
 Db 501 EQMGAELTEQLQ----AVERRIYELAGQEENINSP-----KQLGT---VLFDKLQLPVLKK 549
 Qy 482 FKLGDDYDPMVLSY-----ERVEVYQGSPLAAAATMIGAHVHQASAMOALQKVFSRYYT 540
 Db 550 TKTG-YSTSADVDEKLAPHETIVE-HILHYRQLGKQSTYIE-GLKVVHPVTGKVHTM 605
 Qy 541 RNAEAPXDVQET-----VFSYDVPGVGNNGRDGEPGYFTAAYRPSE-----NFETNDYAI 590
 Db 606 FNQ-----LTOTGRLSSVBNLONIPTIRLBEGRKIRQAFVPSEDDWLIPADYSQIELRV 661
 Qy 591 RAGVSESSVDETVE-----MSVADMIC-----ASVKTLLAAGYAIGLILSFSQ 634
 Db 662 LAHIAE-----DDNLIEAPRGLD1HTKTANDMFHVSEEDYTANNERQAKAVNFGIVYGISD 718
 Qy 635 KYPLKSSSFORKDMVSNESDVATGSGYRADDSEBALPRMDARTAENTISKWOKIKSLAF 694
 Db 719 -YGLAQNUNITRKAEAFFEIEFYFASPGVK-----QYMDNIVQ-B-AKQKGYVT 764
 Qy 695 GPDHRIEMLPVLDGRM-LKIWIDRRA-EAQOLGLVYDYLTLKLISV-SVTVSADGTRA- 750
 Db 765 TLJHRRYLPDTISRFNIVRSFERTAMNTPIQGSAAD-TIKRAMIDLSVRLREERLQAR 823
 Qy 751 -----LVEATLEESACSLDVHPE 769
 Db 824 LLLQVHDELITLEAPCEHEIERLCRLV-PE 850

RESULT 13
 US-08-394-232A-32
 ; Sequence 32, Application US/08394232A
 ; Patent No. 6100078
 ; GENERAL INFORMATION:
 ; APPLICANT: RIGGS, MICHAEL G.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: SIVARAM, MATHOOR
 ; TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILUS
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gen-Probe Incorporated
 ; STREET: 9880 Campus Point Drive
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92121
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/394,232A
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/307,410
 FILING DATE: 16-SEP-1994
 APPLICATION NUMBER: 08/222,612
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: GP94003.CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-7287
 TELEX:
 TELEFAX: 619-546-7929

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
 LENGTH: 876 amino acids
 TYPE: amino acid
 STRAND/DIRECTION: Single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 3-08-394-232A-32

Query Match Score 128 5; DB 2; Length 876;
 Best Local Similarity 21.0%; Pred. No. 0.0056;
 Matches 170; Conservative 135; Mismatches 302; Indels 201; Gaps 43;

Y 99 HPLITGIRRFAEARYSKPPGFSDDALISRQQLAACETLSNPSRREY-NEGILDDE 157
 Y 107 HYADDIIGTMAARAERE---GPAYKVISGDRDLTQ---LASPVQTVTEITKGITDIE 158
 Y 158 EATVITDV-----PMDKPG-----ALCVLQEGEGSTEIVLRVG 190
 Y 159 SPTPTVVERGYLTPEQIVDVLKGMDKSNTIPGVPGIGERTAVKLUJQFGTVENLASI 218
 Y 191 EALLKERPKSKFSQ---DYYLVMLAFLDYSDRA---MALDOPPDFTGTYEFVBEALKLQE 245
 Y 219 DEIKBGEKLKNRQYRDLL-LSKQLAACIRDAPEVLTLD-DIVYKGEDREKVAFQF 275
 Y 246 EGASSLAPDILRQAQIDE-----TLEBITPVYELLG----PLGDDYARKELNG- 290
 Y 276 LGFQSFLDKMAVQTDBEGKPLAGMDFAIDSVTDEMADKAALVVVVGDNYTHAPIVGI 335
 Y 291 ---LSGVRNLTWSVGGGASALVGGLTREKFNEAFLRMTAAE---- 330
 Y 336 ALANERGRFLRPTALADPKFLAW-----LGDETAKTKTMFDKRAAVALKWKG1 385
 Y 331 ----QVDLFVATPSNIPAES-----PEVVEYALVAQAFIGK----KPHLHQ 370
 Y 386 ELRGYVFEDLILAYILDPQAQDVAAVRMHOVEAVRSDEAVYCKGAKRTVPDETLAE 445
 Y 371 DADQFOQOQAOARKNAMEIPAMLYDTTRNWE-IDFGGLERGICALIJG----KVDFCRM 423
 Y 446 HLAR---KAAAIWALEELPMDELRNEODRLLTELEQPLAGILANMEFTGKVDTKRL 500
 Y 424 -WLGHD-SEDSQYRNPAIVEFVLENSNRDDNDLPGLKULTEWLLAGVVPFRDTKDKK 481
 Y 501 EQMGAELITQLOQ---AVERRVYELAGQEFNINSP---KQDG---VLFDRLQLPVLRK 549
 Y 482 FKLGDXDPPMVLSYL-ERVEVQGSPLAAATMARIAGHVKASAMQLQKVPSRYTD 540
 Y 550 TKTG-YSTSADVLEKLAPHEIVE--HHLHYROLGKLOSTYE-GULLKVVHPVTKVHTM 605
 Y 541 RNSAEPLKQVET---VFSVDPVGNVNGRDEBPGVFTAEEAVPSEB-----NFETNDYAI 590

RESULT 14
 US-08-394-232A-34
 ; Sequence 34, Application US/08394232A
 ; Patent No. 6100078
 GENERAL INFORMATION:
 APPLICANT: RIGGS, MICHAEL G.
 APPLICANT: SIVARAM, MATHOOR
 APPLICANT: TUDOR, STARLA D.
 TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS STEAROTHERMOPHILUS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gen-Probe Incorporated
 STREET: 9880 Campus Point Drive
 CITY: San Diego
 STATE: CA
 COUNTRY: USA
 ZIP: 92121
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSSO Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/394,232A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/307,410
 FILING DATE: 16-SEP-1994
 APPLICATION NUMBER: 08/222,612
 FILING DATE: 16-SEP-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Fisher, Carlos A.
 REGISTRATION NUMBER: 36,510
 REFERENCE/DOCKET NUMBER: GP94003.CP2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-535-2807
 TELEX: 619-546-7929

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:
 LENGTH: 876 amino acids
 TYPE: amino acid
 STRANDBDNBS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 US-08-394-232A-34

Query Watch
 Best Local Similarity 3.2%
 Score 128.5; DB 2; Length 876;
 Score 128.5; DB 2; Length 876;

Sequence 20, Application PC/TUS9504080									
GENERAL INFORMATION:									
TITLE OF INVENTION: PURIFIED DNA POLYMERASE FROM BACILLUS						CT-04080-20			
NUMBER OF SEQUENCES: 34						Sequence 20, Application PC/TUS9504080			
COMPUTER READABLE FORM:						GENERAL INFORMATION:			
COMPUTER: IBM PC compatible						TITLE OF INVENTION: STEAROTHERMOPHILUS			
OPERATING SYSTEM: PC-DOS/MS-DOS						NUMBER OF SEQUENCES: 34			
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)						COMPUTER READABLE FORM:			
CURRENT APPLICATION DATA:									
Matches	170;	Conservative	135;	Mismatches	302;	Indels	201;	Gaps	43;
Y	99	HFLTDGIRRAPEARSKPPQFGFSDDALISRROIQAETUSNPRSRREY-NEGILIDDE	157						
b	107	HYADDLIGTNAARAERE--GFAVKVIGSDRDLTQ----LASPQVTEITRKGITDIE	158						
Y	158	EATVITDV-----PWDKVPG-----ALCVLOEGGETEIVLRVG	190						
b	159	SYTPTRVEKYGLTPEQIVDLKGLMGDKSDNITGPVGTGEKAVKLJKQFGTVENVLASI	218						
Y	191	BALLKERLPKSXQ--DVLVIALAFDVSRA---NALDPPDFITGYFVEEALKLQE	245						
b	219	DEIKGEKLLKENRQYRDLA-LSKQLAAICRDPVELD-DIVYKEDRKEVVALQE	275						
Y	246	EGASSLAPDLRQAIDE-----TLEETPTRYVLELLGQ-----KPHLQ	330						
b	276	LGQSFSLDKMAVQTDEBKPLAKMDFAJADSTDEMELADKAALVVVEYGGNTWAPIVG	335						
Y	291	--QVDLFVATPSNPAES-----FEVYEVALLVAQAFIGK-----KPHLQ	370						
b	336	ALANERGRFFLPETALADPKFLAW-----LGDETCKTMFDSKRAAVALKWKGI	385						
Y	331	--QVDLFVATPSNPAES-----FEVYEVALLVAQAFIGK-----KPHLQ	445						
b	386	BLRGVVFEDLLAYLDPAQAGDVAAVAKMHOYEARSDEAVYKGAKRTVDEPTLAE	445						
Y	371	DADKOFQOQQAKVAMAEIPAMLYDTNNWE-IDFGLERGLCALLIG-----KVDECRM	423						
b	446	HLAR-----KAAIAWALEPLMDELRRNEQRDLTTEQPLAGILANMFETGVKDVTKRL	500						
Y	424	-WLGLDD-SEDSYRNPAIVEFTLENSNRDDNDLPGLCKLLETLWAGYVFRFRDTKDKK	481						
b	501	EQMGAELTEQLO---AVERRYYELAGOBNINSP---KQLGT---VLFDKQLPVLUKK	549						
Y	482	FKLGDYDDPMVLSYI-ERVEVYQGSPLAAAATMARIAGEHVKASAMQALQVFPSSRYTD	540						
b	550	TKTG-YSTSADYLEKPHHEVE--HILHYROLKGKLOSTY-GLLKVKVHPPTGKVHTM	605						
Y	541	RNSAEPKDVQET--VFSVDPVGRNVGRDGEPEGYPIAEAVRPE-----NFPTNDVAYI	590						
b	606	FNQA---LTQGRLRSSVEPNLQNPRLLEGKIRQAFVPSSEPDWLIADAQSIELRV	661						
Y	591	RAGVSESSVDETVE-----MSVADMILKE---ASYKILAAQVAGVAGNISLFSQ	634						
b	662	LPHIAE---DDNLIEAFRRLGDIHTKTAAMDIFVSEEDTANRNRQATAVNFGIVGTS	718						
Y	635	KYFLKSSSSFQRKDMVSSMESDVATIGSVRADDSSEALPRMDARTAENYKWKQKIKSLAF	694						
b	719	-YGLAQNINITKKEAAIFIYFASPFPSVK-----QYMDNTVQE-AKQKGIVT	764						
Y	695	GDRHIREMLPEVLDGRM-LKIVITDRAA-ETAQGLVYDYLTLKLSSD-SVTVSADGTRA-	750						
b	765	TILHRRYLPDTTSRPNFNRSAERTAMNTPIQGSAAD-IKXKAMIDLSVRRLBERLQR	823						
Y	751	-----LYBATLLEESACSLSYHPE	769						
b	824	LILQVHDILELAPKEETERLCRLV-PE	850						
Y	835	KYFLKSSSSFQRKDMVSSMESDVATIGSVRADDSSEALPRMDARTAENYKWKQKIKSLAF	694						
b	719	-YGLAQNINITKKEAAIFIYFASPFPSVK-----QYMDNTVQE-AKQKGIVT	764						
Y	695	GPDHRIEMLPEVLDGRM-LKIWTDRAA-ETAQGLVYDYLTLKLSSD-SVTVSADGTRA-	750						
b	765	TILHRRYLPDTTSRPNFNRSAERTAMNTPIQGSAAD-IKXKAMIDLSVRRLBERLQR	823						
Y	751	-----LYBATLLEESACSLSYHPE	769						
b	824	LILQVHDILELAPKEETERLCRLV-PE	850						
Y	835	KYFLKSSSSFQRKDMVSSMESDVATIGSVRADDSSEALPRMDARTAENYKWKQKIKSLAF	694						
b	719	-YGLAQNINITKKEAAIFIYFASPFPSVK-----QYMDNTVQE-AKQKGIVT	764						
Y	695	GPDHRIEMLPEVLDGRM-LKIWTDRAA-ETAQGLVYDYLTLKLSSD-SVTVSADGTRA-	750						
b	765	TILHRRYLPDTTSRPNFNRSAERTAMNTPIQGSAAD-IKXKAMIDLSVRRLBERLQR	823						
Y	751	-----LYBATLLEESACSLSYHPE	769						
b	824	LILQVHDILELAPKEETERLCRLV-PE	850						

Job time : 51 secs

Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,	Qy	481	KPKLGDYDDPMVLSYLERVEVQGSPPLAAATMARIAGEHVKASAMOALQKVPPSRYTD	540
RA Tabata S.,	Db	481	KPKLGDYDDPMVLSYLERVEVQGSPPLAAATMARIAGEHVKASAMOALQKVPPSRYTD	540
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.				
RT Sequence features of the regions of 1,081,958 bp covered by seventeen				
RT physically assigned PI and TAC clones.";				
RL DNA Res. 5:379-391(1998).	RN [12]			
RL Submitted [MAR-2002] to the EMBL/GenBank/DBJ databases.	RN [13]			
RP NUCLEOTIDE SEQUENCE.	DR	06Z729	ORYZA PRELIMINARY;	PRT:
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang B., Dale J.M.,	DR	06Z729_		760 AA.
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,	AC	06Z729_		
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,	DR	05-JUL-2004	(TRMBIrel. 27, Created)	
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,	DR	05-JUL-2004	(TRMBIrel. 27, Last sequence update)	
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,	DR	05-JUL-2004	(TRMBIrel. 27, Last annotation update)	
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,	DR			
RA Sakurai T., Satoh M., Seki M., Shinn P., Southwick A., Shinozaki K.,	DR			
RA Davis R.W., Eckert J.R., Theologis A.,	DR			
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Eckert J.R.,	DR			
RA Theologis A.; Submitted [SEP-2002] to the EMBL/GenBank/DBJ databases.	DR			
DR EMBL; ABO16888; BAB1_0489.1; -; Genomic_DNA.	DR			
DR EMBL; AY091075; AAM13895.1; -; mRNA.	DR			
DR EMBL; AY150490; AAN12907.1; -; mRNA.	DR			
DR GO; GO:0016021; C:integral to membrane; IEA.	GO			
DR GO; GO:0031072; F:heat shock protein binding; IEA.	GO			
DR GO; GO:0051082; F:unfolded protein binding; IEA.	GO			
DR GO; GO:006457; F:protein folding; IEA.	GO			
DR InterPro; IPR001623; DnaJ_N.	DR			
KW Hypothetical protein.	DR			
KW SEQUENCE 801 AA; 88260 MW; 608E776FB#73FECP CRC64;	DR			
Query Match 99.7%; Score 4051; DB 2; Length 801;				
Best Local Similarity 99.8%; Pred. No. 2; e=2.9; Indels 0; Gaps 0;				
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
RN				
RP NUCLEOTIDE SEQUENCE.				
RA Sasaki T., Matsumoto T., Yamamoto K.;				
RA RT "Oryza sativa nippobare (GA3) genomic DNA, chromosome 2, PAC				
RT clone: P0575F10."				
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AP004885; BAD07942.1; -; Genomic_DNA.				
DR Gramene; Q6Z729;				
DR GO; GO:0031072; F:heat shock protein binding; IEA.				
DR GO; GO:0051082; F:unfolded protein binding; IEA.				
DR GO; GO:006457; F:protein folding; IEA.				
DR InterPro; IPR001623; DnaJ_N.				
SQ SEQUENCE 760 AA; 84134 MW;	SQ			
Query Match 43.7%; Score 1775.5; DB 2;				
Best Local Similarity 47.9%; Pred. No. 2.8e-104;				
Matches 3390; Conservative 119; Mismatches 213; Indels 93; Gaps 16;				
RY				
1 MEALSHVGIGLSPFOLCRLPATTKURRSNTTCTCSASKMADRLLSDNFNTSDSSSS 60	1	MEALSHVGIGLSPFOLCRLPATTKURRSNTTCTCSASKMADRLLSDNFNTSDSSSS 60		
1 MEALSHVGIGLSPFOLCRLPATTKURRSNTTCTCSASKMADRLLSDNFNTSDSSSS 60	1	MEALSHVGIGLSPFOLCRLPATTKURRSNTTCTCSASKMADRLLSDNFNTSDSSSS 60		
61 FATTATTTATLVSFSJSDRPRHVPIDFQVQLGAOTHETLDGIRAFEARVSKPQFG 120	61	FATTATTTATLVSFSJSDRPRHVPIDFQVQLGAOTHETLDGIRAFEARVSKPQFG 120		
61 FATTATTTATLVSFSJSDRPRHVPIDFQVQLGAOTHETLDGIRAFEARVSKPQFG 120	61	FATTATTTATLVSFSJSDRPRHVPIDFQVQLGAOTHETLDGIRAFEARVSKPQFG 120		
121 FSDDALISRSQIQLQACETLSNPSRSREYNEGLLDDEBEATVTDPMKDVKPGALCVLQEG 180	121	FSDDALISRSQIQLQACETLSNPSRSREYNEGLLDDEBEATVTDPMKDVKPGALCVLQEG 180		
121 FSDDALISRSQIQLQACETLSNPSRSREYNELDDEBEATVTDPMKDVKPGALCVLQEG 180	121	FSDDALISRSQIQLQACETLSNPSRSREYNELDDEBEATVTDPMKDVKPGALCVLQEG 180		
181 GETETIVLRGEALLKERLPKSFKDQVLYMALAFLDVFYATPSNPAESFEEVYVALVAQA 240	181	GETETIVLRGEALLKERLPKSFKDQVLYMALAFLDVFYATPSNPAESFEEVYVALVAQA 240		
181 GETETIVLRGEALLKERLPKSFKDQVLYMALAFLDVFYATPSNPAESFEEVYVALVAQA 240	181	GETETIVLRGEALLKERLPKSFKDQVLYMALAFLDVFYATPSNPAESFEEVYVALVAQA 240		
241 KLQBEGASSLAQDRAQIDETLEEITPRYVLELLGPQGDYYAARQLNLGSVRNLWS 300	241	KLQBEGASSLAQDRAQIDETLEEITPRYVLELLGPQGDYYAARQLNLGSVRNLWS 300		
241 KLQBEGASSLAQDRAQIDETLEEITPRYVLELLGPQGDYYAARQLNLGSVRNLWS 300	241	KLQBEGASSLAQDRAQIDETLEEITPRYVLELLGPQGDYYAARQLNLGSVRNLWS 300		
301 VGGGGASALYGGLTREKFMNEAFLRMTAAEQDLFYATPSNPAESFEEVYVALVAQA 360	301	VGGGGASALYGGLTREKFMNEAFLRMTAAEQDLFYATPSNPAESFEEVYVALVAQA 360		
301 VGGGGASALYGGLTREKFMNEAFLRMTAAEQDLFYATPSNPAESFEEVYVALVAQA 360	301	VGGGGASALYGGLTREKFMNEAFLRMTAAEQDLFYATPSNPAESFEEVYVALVAQA 360		
361 FIGKPHPLQDADKFOQLOQAKNAMEIPAMLYDTRNNWEIDFGLERGLCLLIGKVDE 420	361	FIGKPHPLQDADKFOQLOQAKNAMEIPAMLYDTRNNWEIDFGLERGLCLLIGKVDE 420		
361 FIGKPHPLQDADKFOQLOQAKNAMEIPAMLYDTRNNWEIDFGLERGLCLLIGKVDE 420	361	FIGKPHPLQDADKFOQLOQAKNAMEIPAMLYDTRNNWEIDFGLERGLCLLIGKVDE 420		
421 CRMWGLDSSEDSQENPAIVFVLNSRNDNDLPLGCKLKEUETWAGVVPRFRDTDKD 480	421	CRMWGLDSSEDSQENPAIVFVLNSRNDNDLPLGCKLKEUETWAGVVPRFRDTDKD 480		
421 CRMWGLDSSEDSQENPAIVFVLNSRNDNDLPLGCKLKEUETWAGVVPRFRDTDKD 480	421	CRMWGLDSSEDSQENPAIVFVLNSRNDNDLPLGCKLKEUETWAGVVPRFRDTDKD 480		

Sequence Alignment Report						
QY_246	EGASSLAPDIRAQLDTEBETTPRVLEILGLPLGDDYAAKRNLNGLSGVNINLNSVGGGG	Score: 43.7%	Length: 760;	DB: 2;	Best Local Similarity: 47.9%;	Prod. No. 2-8e-104;
QY_245	DGASNLPALDISQDDETBETTPRCVLEILSPLIDTEHKKRQEGLQGARNILNSVGRGG	Matches: 390;	Conservative: 119;	Mismatches: 213;	Indels: 93;	Gaps: 16;
QY_306	ASALVGGTIREKEPNNEAFLRMTAAEQLDLYVATPSNIPARSFEVVEVALVAORFIGKK	Query Match: 3.65	SPFQLCRUPPATKLRSRSHNTSTTC-SASKWADRLSDPNEF----TSDSSSSFFATAT	65		
Db_305	IATVGGFSRBAFNUFAUTMNTSIQMDFFSKTPNSIPPWFETIVNALVAQAIIISKR	1.34	AFFAFSLPRPRPRPRPRPPHSACRAASRWAIRLTAAPSPPSAAPAPA	73		
QY_366	PHLIQDAKDFQOLQOAKYNAMEI PAMLYDTDRNWEIDSLERGLCALLIGKVDECRMWL	4.25	TTATLVLSSPSIDRPERRYPIPDIFYQVLGAQATHPLTDGIRRPEARVSKKPOFGESDDA	125		
Db_365	POFIMMADDIEFOLQKENGS---HYAVDN---	1.16	74 APSASPVPFLPDAERSLPLQVDFYKVGAEPFLGDGIRRPEARIAKPOCYSTDA	133		
QY_426	GLDSESDSQYRNPAITVFVLLNSN-RDDNDLPLGCKLLETLWLAGTVFPRFRDTDKKFKL	4.84	1.16 TTATLVLSSPSIDRPERRYPIPDIFYQVLGAQATHPLTDGIRRPEARVSKKPOFGESDDA	125		
Db_417	GIDNESSPYPDKPLEFIVTNNSISIBENDLPLGCKLLETLWLFEVFPRSDRTGMQFRL	4.76	74 APSASPVPFLPDAERSLPLQVDFYKVGAEPFLGDGIRRPEARIAKPOCYSTDA	133		
QY_485	GDXYDDPMVLSYLESERVVEVQGSPAAAATMARIAGAE-----HYUKASAMAOALOKVFP-SR	5.37	1.26 LSRSRQLQAACTTSNPRSRREYNEGGLDDEATETVITDPWDKVPGALCVLQEGGBETEI	185		
Db_477	GDXYDDPMVLSYLESERVVEVQGSPAAAATMARIAGAE-----HYUKASAMAOALOKVFP-SR	5.36	1.34 LVGRQRMLQIAHTDLMMQNSRTQYDRAISENREALTMIDIAWDK-----EAGEALA	184		
QY_538	YTDRNSAEPKDVQETVTFSDPVGNNVGRDGPGPVFTAEEAVRPSNFETNDYAIRGVSES	5.97	1.86 VLRVGEALKERLKPSTFKQDYYVUMLAFLDVSRDAMALDPPDFITGYFVEBALKLQE	245		
Db_537	QLDRSAMEN-----KDG-PGGYL-----ENFDQ-----	5.59	1.85 VLVTGEOQMLDREPDKPFQDVVLAMALAYVDSLRSRDAAMAAPPDYTGCCTEYLRAKLQE	244		
QY_598	SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56	1.86 EGASSLAPDLRQIDEETLEITPRYVLEILGLPLGDDYAKRNLNGLSGVNINLNSVGGGG	3.05		
Db_560	-ENAPAHDSRNRNALKLTISICGALFALLAVIGAKY-----LPRKRPLSAIRSEH	6.05	1.87 206 ASALVGGLTREKFNMNEAFLRMTAAEQLDLYVATVALVAQAFIGKK	3.65		
QY_657	-VATIGSVBADDSEAL-----PRMDARTAENIYSKWKQIKSLAFLGDPDRIEMLPEVJ	7.07	1.88 205 IATVGGFSREAFNMNEAFLRMTTSLEQMDFFSKTPNSIIPPWFEIYNVALVLAHVQATISKR	3.64		
Db_606	GSVAVANSYSTDDEPDLADEDOPVHIFPRMDAKLAEIDYRKWQSIIKSALGPHPSVASHQEVL	6.65	1.89 245 DGSNLNAPLQLSQIDETLEEITPRCVELLSLSPIDTENHKKROBLSQLOGARNILNSVGRGG	3.04		
QY_708	DGRMLKUWTDRAAETAQOLGLYDVTLLKLSUDSVTVAADGTRALVEATLEBSACSLSDLVH	7.67	1.90 246 GLDSEDSYRNPAIVEFTLLENS-RDDNDLPLGCKLLETLWLAGVFPFRPRDFTDKKFKL	4.84		
Db_666	DGMMLKUWTDRAAEIERHGFWWEYTLSDVTDITSLTISLDGRATEATIDEGQLTDVTE	7.25	1.91 365 PHILQDADKQFQQLQQAKWMAAEIPAMLYDTTRNWEIDGLERGLCALLIGKVDECRMWL	4.25		
QY_768	PENNATDVRTTYTRYEVFWSK-SGMWKITEGGSVLAS 801	7.62	1.92 366 PQFIMMADDLFLEQLOQKFNIGS---HYAYDN---EMDIALERAFCSLIVGDSVSKRMWL	4.16		
Db_726	PRNNDSYDTKXTTRYEMAFLSLLGGWKITEGAVLKS 760	7.25	1.93 367 GLDSEDSYRNPAIVEFTLLENS-RDDNDLPLGCKLLETLWLAGVFPFRPRDFTDKKFKL	4.84		
QY_774	RESULT 5	7.62	1.94 417 GIDNESSPYRDPKLEFIVTNSSISEENDLPLGCKLLETLWLFEVFPRSRDTRGMQFRL	4.76		
Q7PC78_0RYSA	SEQUENCE	7.62	1.95 485 GDYXDDPMVLSYLESERVVEVQGSPAAAATMARIAGAE-----HYUKASAMAOALOKVFP-SR	3.65		
ID_Q7PC78_0RYSA	PRELIMINARY;	7.60	1.96 486 537 YDRLNSAEPKDVQETVFSVDPVGNNVGRDGPGPVFTAEEAVRPSNFETNDYAIRGVSES	5.97		
DT_01-MAR-2004	(TREMBLrel. 26, Created)	7.60	1.97 538 YDRLNSAEPKDVQETVFSVDPVGNNVGRDGPGPVFTAEEAVRPSNFETNDYAIRGVSES	5.97		
DT_01-MAR-2004	(TREMBLrel. 26, Last sequence update)	7.60	1.98 539 537 QLDRSAMEN-----KDG-PGGYL-----ENFDQ-----	5.59		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	1.99 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.00 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.01 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.02 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.03 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.04 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.05 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.06 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.07 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.08 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.09 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.10 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.11 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.12 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.13 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.14 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.15 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.16 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.17 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.18 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.19 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.20 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.21 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.22 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.23 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.24 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.25 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.26 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.27 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.28 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.29 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.30 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.31 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.32 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.33 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.34 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.35 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.36 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.37 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.38 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.39 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.40 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.41 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.42 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.43 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.44 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.45 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.46 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.47 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.48 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.49 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.50 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.51 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.52 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.53 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.54 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.55 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.56 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.57 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.58 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.59 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.60 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.61 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.62 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.63 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.64 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.65 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.66 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.67 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.68 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.69 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.70 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.71 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.72 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.73 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.74 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.75 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.76 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.77 540 539 538 SVDETTVEMSVADMILKEASYKTIILAAGVAIGLISLSQKYTLKSSSFORKDMVSSMESD-	6.56		
DT_01-MAR-2004	(TREMBLrel. 26, Last annotation update)	7.60	2.78 5			

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	DR HSSP; P08622; 1BQZ.
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	GO; GO:0031072; F:heat shock protein binding; IEA.
OX [NCBI_TaxID=3702;	GO; GO:0051082; F:unfolded protein binding; IEA.
RN [1]	DR
RP NUCLEOTIDE SEQUENCE.	DR
RX MEDLINE=22779057; PubMed=12897262; DOI=10.1105/tpc.013292;	DR
RA Vitha S., Froehlich J.E., Kohsharova O., Pyke K.A., Van Erp H.,	DR
RA Osteryoung K.W.;	DR
RA "ARO6 is a J-domain plastid division protein and an evolutionary	DR
RT descendant of the cyanobacterial cell division protein Ftn2.";	DR
RT Plant Cell 15:1918-1933 (2003).	DR
EMBL: AY221467; AAQ18644.1; -; Genomic_DNA.	DR
DR ; GO:001021; C:integral to membrane; IEA.	DR
DR ; GO:0031072; F:heat shock protein binding; IEA.	DR
DR ; GO:0051082; F:unfolded protein binding; IEA.	DR
DR InterPro: IPR001623; DnaJ_N.	DR
DR ; GO:0006457; PheoN.	DR
DR InterPro: IPR001633; DnaJ_N.	DR
SQ SEQUENCE 324 AA; 35168_MN; OCC5C0CC469A6325 CRC64;	DR
Query Match 40.5%; Score 1646; DB 2; Length 324;	DR
Best Local Similarity 100.0%; Pred. No. 1..4e-96;	DR
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR
Qy 1 MEALSHVGGIGSPOLCRUPATPKLRRSHNTSTTCASKWARRLSDPNFTSDSSSS 60	Db 71 KERSSYDOLYLAHAYDDNAATTKVAVENRQDSNNHFDVOSLSI-EVSSSEBLIGALLI 128
Db 1 MEALSHVGGIGSPOLCRUPATPKLRRSHNTSTTCASKWARRLSDPNFTSDSSSS 60	Qy 177 LQEGETTEIVLRVGELL-----KERLPKSF----KQDVVLVNLALAFDVSR 219
Qy 61 FATTATTATLVSLLPSIDEPRHYPIDFYQVIGAQTHFLTDGIRRAFARYSKPPQG 120	Db 129 LQELGEYELVLLKGNLYLGNQNGTASTRNGHNRTPBEFLDSSERPDILTVALLASLEIGR 188
Db 61 FATTATTATLVSLLPSIDEPRHYPIDFYQVIGAQTHFLTDGIRRAFARYSKPPQG 120	Qy 220 D-----AMALIPDPDFITGYEYVEALKLQLQEGASSLAPDRAQIDETLEETTPR 269
Qy 121 FSDDALISRRQILOAACETLNSNPRSRNEYNEGLDDBEATVITDVPWDKPGALCVLQG 180	Db 189 EQWQOQHYENALSLF---TGQE-----VLFSEG---IPTSYQAEIQADLYKURPY 233
Db 121 FSDDALISRRQILOAACETLNSNPRSRNEYNEGLDDBEATVITDVPWDKPGALCVLQG 180	Qy 270 YVLELLGLPLGGDYAAKRNLNGLSGVNINLMSVGG-GGASALVGGLTRE--KFMNEAFLR 325
Qy 181 GETEIVLVRGEALLKERLPKSFQDVVLYMALAPDPPDTGYEFVERAL 240	Db 234 RILELLALP-QEKTERHQGLDLIQLSILDQRGIGTGTNDQGLNIDDFRFIOQLRH 291
Db 181 GETEIVLVRGEALLKERLPKSFQDVVLYMALAPDPPDTGYEFVERAL 240	Qy 326 MTAALQDVLFWATPSNIPASSPEVYEVALLVAQF1GKPHLQDAKDQPOQLOQAKVM 385
Qy 241 KLIQBEGASSLAPPRLQIQTDELITPRYVLELLGLPQDDYAAKRNLNGSGVNLIMS 300	Db 292 LTVABOQKLFDG-ESKRPS-AVATVIAVYASIAARGTQRQPALIRAKQILMRSRQ-- 347
Db 241 KLIQBEGASSLAPPRLQIQTDELITPRYVLELLGLPQDDYAAKRNLNGSGVNLIMS 300	Qy 386 AMEPAMLYDTTRNNWBDLFGELRGCLIGKVDERCMWLGIDSEPSQYRPAIVEFVLE 445
Qy 301 VGGCGASALVGG3LTREKPMNEAFL 324	Db 348 -----DVHLEQSLCALLIGQTEETTRLVLSQE--YEALALI---R 383
Db 301 VGGCGASALVGG3LTREKPMNEAFL 324	Qy 446 NSNRDDNDLPLGLCKLLETWLAGVVFPRFRDTDKKKFKLGDYYDDPMWLSLERV---- 500
Qy 541 RNSAEPKDYQETVSVDFPVGNNVGRDE-----PGVFAEAVRPSNFETND 587	Db 384 EKSQDPSPDLLPGLCLIXAEQWLNQNEVFPHERFDLSRQASLKDYFANQVOQAYALEALPNDAE 443
Db 504 QNRPPDPELPETSNRPPSNFTARENISTTDAYTDNYPPPEIPBRASP----- 555	Qy 501 -----EVQGSPLAIAAMAR--IGAEEH-VKASAMQALQKVPPS--RYTD 540
Db 588 YAIRAGVS--ESSVDETTV----- 555	Db 444 TTNEAVINRQFSOSQRGNSYSGGTPVAKPVGKARPGEASTRPPQRSHPSVNQFQH 503
Qy 541 RNSAEPKDYQETVSVDFPVGNNVGRDE-----PGVFAEAVRPSNFETND 587	Db 556 --VQPGVSGTQSTPRQTFKRRERKPKQAVNVRGHSIHQORQSPSTLGRKTRLLWIVL 613
Db 504 QNRPPDPELPETSNRPPSNFTARENISTTDAYTDNYPPPEIPBRASP----- 555	Qy 623 GVAIGLISLFE---SQKY_FLKs---SSSFQKDMVSSMSDVATIGSVADDSSALPR 673
Db 588 YAIRAGVS--ESSVDETTV----- 555	Db 614 G-SLGGILFWLVSTFGMLKNVFPAPSLOGEOLSIQISQPPLEIPDKNAQIQSPEVS 672
RESULT 7 QBYTLO_ANASP ID QBYTLO_ANASP PRELIMINARY;	Db 674 MDARTAENIVSKWOKIKSLAFGPDRHEIPEVLDGRMLK1WTDRAEATAQLGLVYDTL 733
AC	RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
DT 01-MAR-2002 (TREMBLe1. 20, Created)	RA Kishida Y., Kohara M., Matsumoto M., Murakami A., Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yasuda M., Tabata S.,
DT 01-MAR-2002 (TREMBLe1. 20, Last sequence update)	RA
DT 01-JUN-2003 (TREMBLe1. 24, Last annotation update)	RA
DE All12707 Protein.	RA
GN OrderedLocusName=a112707;	RA
OS Anabaena sp. (strain PCC 7120).	RA
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.	RA
OX NCBI_TaxID=10369;	RA
RN [1]	RA
RP NUCLEOTIDE SEQUENCE.	RA
RX MEDLINE=1155285; PubMed=11759840;	RA
RA Kaneko T., Nakamura Y., Sasamoto S., Kuritz T., Sasamoto S.,	RA
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,	RA
RA Kishida Y., Kohara M., Matsumoto M., Murakami A., Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,	RA
RA	RA
RT Complete genomic sequence of the filamentous nitrogen-fixing	RA
RT cyanobacterium Anabaena sp. strain PCC 7120.;"	RA
RL DNA Res. 8:205-213 (2001).	RA
DR EMBL: BA000019; BAB74406.1; -; Genomic_DNA.	RA
DR PIR: AD2144; AD2144.	RA
Qy 791 WKI 793	RA

Query Match	Score	DB	Length
Best Local Similarity	10.9%	Score 442;	DB 2;
Matches 189;	24.5%;	Pred. No. 2, 1e-19;	
Conservative	118;	Mismatches 264;	
Matches 189;	24.5%;	Indels 204;	Gaps 30;
Qy 86	IPIDFYQVQLGAOTHLFTGIRRAFEARVKSPKPPQFGFSDALISRROQLQAACETLSRSPRS 145		
Db 3	IPIDYRILICVGVQASDRKLINQNSPHEFSELALQARROLEAAIAELSDPEQ 62		
Qy 146	RREYNE----GLIDDEBATVITDVPWDKVGALCIVLQEGGETEIVLRGEALL-----194		
Db 63	RDRYDRRRFFQGLEAIESLEED--NORI-GALLLLELGEBYDRVSOLAELLPDYDAS 119		
Qy 195	KERLPKSFKQDVYLVMALAFLDVSRDAMALDPDFITGYEFVEEALKLQERGA-----248		
Db 120	AEVRDQFARGDIALAIALSQQSLIGRCRQ-----OSLYBAAQHGRS 162		
Qy 249	-SSLA-----PDLRAQIDETLEBITPRYVLELGLPDDYAAKRNLNGSGYRNIL-----W 299		
Db 163	QSALADHORFPEPLSRTHQEQQCLQRPLRILAQPLTAD--SDRQGQLLIIQAMLDLDRQ 220		
Qy 300	SVGGGASALVGCLTRKEFMNEAPRL----MTAAEQVDF---VATPSNTPAESPEVYB 351		
Db 221	CIEGPDDG--SGLTLDNFL--MFLQDQIRGYLTLCACQLLFESEARRPS--PAASF----F 271		
Qy 352	VALVALVAQAFIGRKPHILQDAKQFOQOLOQAKVMAAEIPAMLYDTTRNNWEIDFGLERGLC 411		
Db 272	ACYTLIARGFCDHQPSLTHRSSLILHLKS-----RMDVRIQIA 312		
Qy 412	ALLIGKUDCECRMWGLDSED---SQYRNPAIVEFYLENSNRDDNDLPLGJCKLKLTSTWLA 467		
Db 313	SUHLGPOPEEAAIL-VQSQDEETLSQLTRALLQGEAL-----IVGLCRFTTWLA 360		
Qy 468	GVVFPRPFDKDKKFVKGDYTDPMVLSYLERVEVVQGSPLAAAATMARIAGEHYRASAM 527		
Db 361	TKVFPDPFDLKERATPLQPYFDPPDQTYLDAIVE-----396		
Qy 528	QALQKTVPPSRYIDRNNAEPKDVQETVYESVDP-----VGNVNNGRDCGPVGFIABAVRPS 580		
Db 397	PSDLMPITPLPVEPLEVRSSLAKELPTPATPG-----VAPP 432		
Qy 581	ENPETNDYAIRAGVSESSVDETTVENSVDADMILKEASYKILLAGVAGLISLESQKVLK 640		
Db 433	PRRRRURSERPARTAKRLPLPWIGLV-----VVVVLGGGTGV-----WAWRS 475		
Qy 641	SSSFQRKDMVSSMSEVATIGSVRAODSEALP-----RMDARTAENTIVSKWOKIKS 691		
Db 476	RSN-----SPPTTPPPVVTQLPEAVPAPSAPPTVALDRAQAEVTLNQWIAAKA 524		
Qy 692	LAFGPDRHIEMLPEVLDGRMLKWTTRAESTA--QIGLVVYDTYLKLSDSYTVTSADGTR 749		
Db 525	AALGPQYDRDRLLATVTEGVLTQWQFSQANTOLTSOPDH--KLTVDVSQLSGDQDQ 581		
Qy 750	ALVATELLESAACLSDIVHPENNATDVT--YTTRYEVFWSKGWNWITEGSQL 799		
Db 582	AVVQAVKDE---VEQVYRGDOLLETFRDLGLVIRYQLVRENNNIKIASILV 630		
RESULT 10			
Q5N039_STNP6	PRELIMINARY:	PRT:	631 AA.
Q5N039_STNP6			
AC	Q5N039;		
DT	01-FBB-2005 (TREMBLrel. 29, Created)		
DT	01-FBB-2005 (TREMBLrel. 29, Last sequence update)		
DT	01-FBB-2005 (TREMBLrel. 29, Last annotation update)		
DB	Cell division Protein Ptn2 homolog.		
OrderedLocusNames	=syn2151_d;		
GN	Synechococcus sp. (strain PCC 6301) (<i>Anacystis nidulans</i>).		
OS	Bacteria; Cyanobacteria; Chroococcales; Synechococcus.		
OC			
OX			
[1]			
RN	NUCLEOTIDE SEQUENCE		
RP			
RA			
RT	"Complete genome structure of the unicellular cyanobacterium <i>Anacystis</i> Sugita M.;		

Qy	581	ENPETNDYAIRGVSESSVDETTVENSYADMILKBAVSUKILAAAGVAILLISFQKYFLKS	640	Qy	391	AMLYDDPRNNWEIDFGERGLCALLIGKVDECRMWGL-----DSESDQRNPAIVEPVLEN	444
Db	433	PRRRRURSERPARTAKRLPLWIGLGY-----VVVGGGTGTV-----WAWS	475	Db	397	A-----SEGDLKLPEAFCSFLLKQGEAELBKQLENSDSAVRN-----ILGK	444
Qy	641	SSSFQRKDMVSMNESDVATIGSVRADDSELP-----RHDARTAEIVSRWKIKS	691	Qy	447	SNRDDDDLPLGCKLLELTWLAGVFRPRDTK-----DKKFPLGDDYDPMPVL	494
Db	476	RSN-----STPTPPVQTQLPEAVPAPVTVTSDVYADGTR	749	Db	445	E8RSTS-----ATPSLEAWLNEVSLIANPDTGCGSPSLANPRAEKYYPENKGKGSPLSIM	499
Qy	692	LAFGPDHRIEMPEVUDGRMLKIWTDRAAETA---QGLIYVDXTLKLSDVSYTSDVYADGTR	749	Qy	495	SY-----LERVEVVGSPSPLAAAATMARIAGEHVKASAMOALQKVPEPSRTYDRNAEPKD	548
Db	525	AALGPQYDRDLRATLVTLGEVLOIWGFSQQANTQTSQFDH---KLVTDVSYOLSDGQR	581	Db	500	NHKTNQRPLSTTQFVNNS-----QHL-----YTAVEBQLTPD	531
Qy	750	ALVEATLEESACLSLDTYHPPNNTADVRT----YTRYEVFWSSGWKITEGSQL	799	Qy	549	QVETVSVDPVGNNVGRDGEQVFIABAVRPSSENFTNDYARAGVSSSSV-DETTEVMS	607
Db	582	AVYQAKYDE---VEQVYRGQOLLETEDLGLVTRYOLVRENNIWKLASISLIV	630	Db	532	LQSPVYSAK---NNDE-----TSASMPSVQVKEN-----LGVHNKQKIDEW--LS	571
Qy	808	VADMLKEASVTKILLAAGVAGIAIGLISLFLSFCRY-----	636	Qy	608	VADMLKEASVTKILLAAGVAGIAIGLISLFLSFCRY-----	636
Db	572	QSSLIGRGRVVAV-----LGCTVFFSLKLSGRSRQLQSMPSVSRPHSESDFLWKT	626	Db	572	QSSLIGRGRVVAV-----LGCTVFFSLKLSGRSRQLQSMPSVSRPHSESDFLWKT	626
Qy	637	--FLKSSSFQRKDNVSS-----MESDVATIGSVRADDSSEALPR	673	Qy	637	--FLKSSSFQRKDNVSS-----MESDVATIGSVRADDSSEALPR	673
Db	627	SGNFRNKLDSVNRNGIVGNIRKLDMLKMHCGEHPPDALYLKSSQSATSLSHASELHHR	686	Db	627	SGNFRNKLDSVNRNGIVGNIRKLDMLKMHCGEHPPDALYLKSSQSATSLSHASELHHR	686
Qy	674	-MDARPAAENTVSKWQKIKSLAFGPDRIEMLPEVLDGRMLKWTDRAAETAQLGLVY-DY	731	Qy	674	-MDARPAAENTVSKWQKIKSLAFGPDRIEMLPEVLDGRMLKWTDRAAETAQLGLVY-DY	731
Db	687	PMDTEEAELVROWENVKAEALGPHTQVYSLSEBLMSMLVQW-QTLAQTAEAKSYWRF	745	Db	687	PMDTEEAELVROWENVKAEALGPHTQVYSLSEBLMSMLVQW-QTLAQTAEAKSYWRF	745
Qy	732	TLLKLSDVSDTIVSAD---GTRALVATELEESACSLDVLHPENNATDVRYTYTRYEVFWSK	788	Qy	732	TLLKLSDVSDTIVSAD---GTRALVATELEESACSLDVLHPENNATDVRYTYTRYEVFWSK	788
Db	746	VLLHLLEVQLQAHIFBDGIAGEARAEIALLBEAELVIDESQPK-NAKYSTYKIRYILRKQE	804	Db	746	VLLHLLEVQLQAHIFBDGIAGEARAEIALLBEAELVIDESQPK-NAKYSTYKIRYILRKQE	804
Qy	789	SG-WKLTGEHSV	798	Qy	789	SG-WKLTGEHSV	798
Db	805	DGLWKRCQSDI	815	Db	805	DGLWKRCQSDI	815
Qy	12	RESULT 12		Qy	Q55559	SYN13	
AC		ID Q55559; SYN13		AC	Q55559;	SYN13	PRELIMINARY;
DT		DT 01-NOV-1996 (T-FEBMBLrel. 01, Created)		DT	01-NOV-1996 (T-FEBMBLrel. 01, Created)		
RA		RA 01-MAR-2002 (TREMBLrel. 20, Created)		DT	01-NOV-1996 (T-FEBMBLrel. 01, Last sequence update)		
RA		RA 01-MAR-2002 (TREMBLrel. 20, Last sequence update)		DT	01-NOV-1996 (T-FEBMBLrel. 01, Last sequence update)		
RA		RA 01-OCT-2003 (TREMBLrel. 25, Last annotation update)		DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE		DE Hypothetical protein At3g19180.		DE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
GN		GN Name=At3g19180;		GN			
OS		OS Arabinidopsis thaliana (Mouse-ear cress);		OS			
OC		OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids; eurosids III; Brassicales; Brassicaceae; Arabidopsis.		OC			
QC		QC		QC			
NCBI_TAXID		NCBI_TAXID=3702;		NCBI_TAXID			
RN		NUCLEOTIDE SEQUENCE		Qy	789	SG-WKLTGEHSV	798
RA		Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,		Qy	789	SG-WKLTGEHSV	798
RA		Goldmuntz A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,		Qy	789	SG-WKLTGEHSV	798
RA		Carminali P., Chen H., Cheuk R., Hayashi Y., Ishida J., Jones T.,		Qy	789	SG-WKLTGEHSV	798
RA		Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,		Qy	789	SG-WKLTGEHSV	798
RA		Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,		Qy	789	SG-WKLTGEHSV	798
RA		Seiki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,		Qy	789	SG-WKLTGEHSV	798
RA		Theologis A.; Theologis A.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.		Qy	789	SG-WKLTGEHSV	798
DR		DR Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.		Qy	789	SG-WKLTGEHSV	798
KW		KW Hypothetical protein.		Qy	789	SG-WKLTGEHSV	798
SEQUENCE		SEQUENCE 819 AA; 90750 MW; 6720083F4864657E CRC64;		Qy	789	SG-WKLTGEHSV	798
Qy		Query Match Similarity 10.6%; Score 431; DB 2; Length 819;		Qy	789	SG-WKLTGEHSV	798
Best Local Similarity 23.5%; Pred. No. 1.6e-18; Matches 200; Conservative 116; Mismatches 311; Indels 224; Gaps 32; OC		OC Bacteriota; Cyanobacteria; Chroococcales; Symeobacteriia; NCBI_TaxID=1148;		Qy	789	SG-WKLTGEHSV	798
DR		DR NUCLEOTIDE SEQUENCE		Qy	789	SG-WKLTGEHSV	798
RX		RX MEDLINE=97061201; PubMed=8905231;		Qy	789	SG-WKLTGEHSV	798
RA		RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirose A., Sugita M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Naruo K., Okumura S., Shimpou S., Takeuchi C., Wada T., Yamada M., Yasuda M., Tabata S.,		Qy	789	SG-WKLTGEHSV	798
RA		RA "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC 6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.", RT DR RNA Res. 3:109-136 (1996)		Qy	789	SG-WKLTGEHSV	798
RA		RA DR EMBL:AY0774283; AAU65980.1; -; mRNA.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR IntPro: IPR01623; DnaJ_N.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR Pfam: PF00226; DnaJ_N.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR SMART: SM00271; DnaJ_1.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR PROSITE: PS50016; DnaJ_2.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR Chaperone; Complete proteome.		Qy	789	SG-WKLTGEHSV	798
RA		RA DR SEQUENCE 714 AA;		Qy	789	SG-WKLTGEHSV	798
DR		DR GO: 0005515; F:protein binding; IPI.		Qy	789	SG-WKLTGEHSV	798
DR		DR GO: 0000917; P:protein binding; IPI.		Qy	789	SG-WKLTGEHSV	798
DR		DR InterPro: IPR01623; DnaJ_N.		Qy	789	SG-WKLTGEHSV	798
DR		DR Pfam: PF00226; DnaJ_N.		Qy	789	SG-WKLTGEHSV	798
DR		DR SMART: SM00271; DnaJ_1.		Qy	789	SG-WKLTGEHSV	798
DR		DR PROSITE: PS50016; DnaJ_2.		Qy	789	SG-WKLTGEHSV	798
DR		DR Chaperone; Complete proteome.		Qy	789	SG-WKLTGEHSV	798
DR		DR SEQUENCE 714 AA;		Qy	789	SG-WKLTGEHSV	798

Query Match	10 6% ; Score 429; DB 2; Length 714;	Best Local Similarity 25.1%; Pred. No. 1.7e-18;	Matches 194; Conservative 124; Mismatches 331; Indels 124; Gaps 30;
Qy	86 IPIDPYQVLAQTHLTGDGFEARVSKPQFGRSDDALISRQDQLQACETLSNPRSPRS 145 3 IPDFFYRILGIP PQSGGETEQAYQDRILLQPLRRESDAATLNRNLLATYETLRDPEK 62	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC and BAC clones." Nucleotide Sequence. [2]
Db	146 RRENEY--GLLDB--EATVTDYEWDKVY--GALCVLQEGGETEIVTRGEAHLKE 1.96 63 RQADQEWWGAMDEALGEALP.LTTPLLECSPEQTGALLTILLDGHYELVYKGPVTLHD 122	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; Submitted (SBE-1999) to the EMBL/GenBank/DBJ databases. EMBL; AP000419; BAB2958.1; -; Genomic DNA.
Qy	197 RLPKS--FKODVVLWMAFLPDVSDAMALDPDFITGYEEVEA-LKLLOEGASSLAP 253 123 PNPPAGGLPDPDYLSSVILAHWELSRWQQQ--YEFATASLISKALARLQQNDFP 176	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	254 DLRAQIDETIEEITTRYVIELLGLP-LGDDYYAKRLANGLSCVRNTILWSVCG-GGASALVG 311 177 ALENEIRQELYRRLRRLLEAKEGGEE--QHQGLLAAVQANVQDRGEGIEGKBEDYS 233	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Query Match 10.5%; Score 425; DB 2; Length 841; Best Local Similarity 23.0%; Pred. No. 4e-18; Matches 200; Conservative 122; Mismatches 308; Indels 240; Gaps 35;
Qy	312 GLTRE--KPMNEAFLRMTAAEQVDLFVATPSNIPAESFVEYEVALLVAQAPIGKPKHL 368 234 GLGNDDEFLRPTIHLQRCHLTVTAQNQFL--PESQPSLIVASYLAHSLMAGEVKEDPMA 291	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	369 LQDADKOFQOOLQOKXMANEIAPAMLYDTRNNWEIDFGLERGLCALLIGKYDECRMWGLD 428 292 IVEAKSLTIOLENCO-----DLAEBKVICELLQGTEV--VLAIAID 330	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Query Match 10.5%; Score 425; DB 2; Length 841; Best Local Similarity 23.0%; Pred. No. 4e-18; Matches 200; Conservative 122; Mismatches 308; Indels 240; Gaps 35;
Qy	429 SEDSOYRNPAIVEPVTLENSNRDDNDLPLGCLKLLETWLQAGVPPFRDTDKKFKLGDYY 488 331 QGD----PKIVA-GLESKLATGEPPLTARYTFTQWLEEIVPPFRDLSPETLSPKAYF 384	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	489 DDPNVLSYLERVTVQ-----GSP-LAAATMAMARIGAHHVKASAM-QALQKVFPSSRYT 539 385 NNPVSQVQIIEQLELPDPSFTTDNSFSPALISTATBSETPMVHSALALPDRPTSTVFS--- 441	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Query Match 10.5%; Score 425; DB 2; Length 841; Best Local Similarity 23.0%; Pred. No. 4e-18; Matches 200; Conservative 122; Mismatches 308; Indels 240; Gaps 35;
Qy	540 DRNSAEPKDVQEVTFSVDPVGNNYGRDGEPEGVFLAEAVRPSENPFTNDYAIRA----- 592 442 -RGRSPSPRSRDRDVF-----SADNSSGLAV-TLSPALAYDTHSLGIGGDSSTS 491	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	593 -GVSSESSVDETTEV-MSVADMLKEASVK-----ILAGVAGLISLFSOK----- 635 492 NGFSSNSAESTSKHKSPPRRKRKVTKPVRGIFPLCLAGIVGGATALLINTRTGDPGLG 551	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Query Match 10.5%; Score 425; DB 2; Length 841; Best Local Similarity 23.0%; Pred. No. 4e-18; Matches 200; Conservative 122; Mismatches 308; Indels 240; Gaps 35;
Qy	636 -----YPLKSSSSFORKDMVSSMESDVATIGSVRADDSSEALPREMDARTAENIVSKWQK 688 552 LLBDPDLV-----DQPSEFTPDEATSRNLILSQ---PWFNQOQVGMVYQGWLD 598	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	689 IKSLAFGPDHRIEMLPEVDGRMLKIWTDAEATAQGLYDVTLLKSYSDSTVTS-ADG 747 599 SKCLAFGQONYDVGALOSVLAQNLAAQRGR-AQDQAQKRYHQYEHKLQQLAYQNPQDP 657	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	Query Match 10.5%; Score 425; DB 2; Length 841; Best Local Similarity 23.0%; Pred. No. 4e-18; Matches 200; Conservative 122; Mismatches 308; Indels 240; Gaps 35;
Qy	748 TRALVEATLLEESACISDLVHPENNATDVR-TYTRYEYFWKSGMKITEGSVL 799 658 NRATVTARVEEISOPFTLNQQKGQSATKDLTVRYQLVRHQGWKIDQIQVV 710	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	SEQUENCE 841 AA; 93216 MW; 7DBEBE72618EE8B97 CRC64;
Db	RESULT 1.3 Q9LJL2_ARATH PRELIMINARY; ID Q9LJL2_ARATH AC Q9LJL2; DT 01-OCT-2000 (TREMBLre1. 15, Created) DT 01-OCT-2000 (TREMBLre1. 15, Last sequence update)	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	DBSEALR -MDARTAENIVSKWQKIKSLAFGDPDHRIEMLPEVDLGRM-----LK 713 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVI11. Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis; [1] NCBI TaxID=3702; NUCLEOTIDE SEQUENCE.
Qy	537 RYTDNRSAEPKDVOETFVSDPVGNVGRDGEPEGVFLAEAVRPSENPFTNDYAIRGVS 596 533 -YTAVEQLTPTDLOSPVSAK--NNDE-----TSAMSPSVQLRN----LGVHK 574	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	DB 575 NKLDEWW--LSQSSLIGRVVALLGCTVFFSLKLGSITRSGLQSMPIVSARPHESED 631 635 KYFLKSSSFQRKDVMSSMESDVATIGSVRA-----SQ 634 632 SFLWKTESENPRKNLDSVNRNGI - VGINIXKVLIDMLKMHCCHEPDAILYKSSGQSATSL 689 635 KYFLKSSSFQRKDVMSSMESDVATIGSVRA-----SQ 634 632 SFLWKTESENPRKNLDSVNRNGI - VGINIXKVLIDMLKMHCCHEPDAILYKSSGQSATSL 689 666 -DBSEALR -MDARTAENIVSKWQKIKSLAFGDPDHRIEMLPEVDLGRM-----LK 713 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVI11. Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis; [1] NCBI TaxID=3702; NUCLEOTIDE SEQUENCE.
Db	714 IWTDRAAETAQQLGVY-DYTLKLUSVSDTVSAD--GTRALVEATLLEESACISDLVHPE 769 750 QW-QTLAQTAEEKSCYFVLLHLEQVHAFEDGIAGEAEIEALLEERAELVDESQPK 808	RRA RTT RTT RTT RTT RN RN RP NUCLEOTIDE SEQUENCE.	DB 750 QW-QTLAQTAEEKSCYFVLLHLEQVHAFEDGIAGEAEIEALLEERAELVDESQPK 808

Qy	770 NNATDVRYTRYFWFKSG-WKITEGSV 798	Qy	195 KERLPKSFQ-----DVLYMVALAFLDVSRDAMALDPDFITGYEFVBEALKLJL 243
Db	809 -NAKYKSTYKTRYILKQQDGILWKFCSODI 837	Db	123 KRDV--PERNPRTSPAVADLTIVTAYDELGREW--QEQSYESMASQLDAGLQVL 177
RESULT 14		Qy	244 QEEGASSLAPDLRQIQTETLEETTPRYVLELLGLPGLGDYAAKRLNGLGSVNRNLWSVGG 303
Q8DKU7_ SYNE1 PRELIMINARY;	PRT; 673 AA.	Db	178 QR--VNLFPELQEOPFOTELNLRPYRILLEALPLSD--SANRQRGIGILLRQMLSERGG 232
ID Q8DKU7;		Qy	304 -GCAASALVGGLIRE--KFMDNEAFLRNTAAEQVDLFTATPSNPAESPEVYEVALLVAQ 359
AC DT 01-MAR-2003 (TRIMBLrel. 23, Created)		Db	233 TEGRQDDRSGLTVEDFLKFILQRLSHLTVAEQELF-----EERRRPSAVATLVAVH 285
DT 01-MAR-2003 (TRIMBLrel. 23, Last sequence update)		Qy	360 AFIGKRPHLQD---ADKQFCQLQAKWMAMBIPAMYLYDTRNNWEDFGLERGLCALL 414
DT 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)		Db	286 ALVARGWHQLPSYICRAKDLQL-----DVYLELASCLL 326
DB Tlr0758 protein.		Qy	415 IGVKDECRRMLGLDSESDQSYRNPAIVEFVYLENSNRDNDLPLGICLKLLTWTLAGVVFPRF 474
GN OrderedLocusNames=t1r0758;		Db	327 LGQPTE----ALAALDHSQDQFLT-DFIRRHAG-EAGDRPLGLEYYYTQWLTEB1YPAF 379
OS Synechococcus elongatus (Thermosynechococcus elongatus).		Qy	475 RDTKDKFKEFLGQDYYDDPMVLSLERYEVVQGSPLAAATMARGAETHVKASAMOALQKVF 534
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.		Db	380 RDGTGETPVALEYFADANVQTYLSEADSDIAPEPPPTA-----
RN NCBI_TaxID=32465;		Qy	535 PSRYTDNSAEPKDXDQETVFSVDPGHNVGRDGPQTAEAVRPSENFTNDYAIRAGV 594
RP NUCLEOTIDE SEQUENCE.		Db	420 -----SALPVPVPTV-AVPP-----PLQDSRSLGGCGSASA 459
RC STRAIN=BP-1;		Qy	595 SRESSVDETTVEMSVADMLKEASVK-----IIAGAVA-IGLISLFSOKYFLKSSS 642
RX MEDLINE=22225144; PubMed=12240834;		Db	460 FTFSATATGTGTSMEQPSPRKRSAQKRQTRWFMWGRGVVVLVGAL--AKYVWPAK 517
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,		Qy	643 SFORKDNVSSMSDVTAGTSVRAADDSEAL---PRMDARTAENIVSKWQKIKSLAFGDHR 699
RA Watanabe A., Iriuchi M., Kashima K., Kimura T., Kishida Y.,		Db	518 ARAPPPTVPAFPVPAFTPTPPTOPTTIAITLTPEM---ARDLHTWQIKAQQLGRPFE 573
RA Kiyokawa C., Kohara M., Matsuno A., Nakazaki N.,		Qy	700 TMLPEYLDGRMKIKTWIDTRAETAOLGHVYDFTKLKSVDTSVTS-ADGTRALVE---A 754
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;		Db	574 VDKLTTIAEPLESRSWRWRAQGLKSBESYVVTLKLNLEVKEYLQRSDRVEVLAENEDA 633
RT "Complete genome structure of the thermophilic cyanobacterium		Qy	755 TLEBSACLSDLVHPENNATDVRYTTRYEWNS 787
RT Thermosynechococcus elongatus BP-1.";		Db	634 RFYEQGTI-----RTDI-SYSDDPVRVITY 656
RL Res-1:123-130 (2002).		RESULT 15	
CC FUNCTION: Participates actively in the response to hyperosmotic		QTV0H1 PROMP	
CC and heat shock by preventing the aggregation of stress-denatured		1D QTV0H1 PROMP PRELIMINARY;	PRT; 702 AA.
CC proteins and by disaggregating proteins, also in an autonomous,		AC QTV0H1;	
CC dnaK-independent fashion. Unfolded proteins bind initially to		DT 01-OCT-2003 (TRIMBLrel. 25, Created)	
CC dnaJ, upon interaction with the dnaJ-bound protein, dnaK		DT 01-OCT-2003 (TRIMBLrel. 25, Last sequence update)	
CC hydrolyzes its bound ATP, resulting in the formation of a stable		CC 01-MAR-2004 (TRIMBLrel. 26, Last annotation update)	
CC complex. GrpE releases ADP from dnaK, ATP binding to dnaK triggers		DE Hypothetical protein.	
CC the release of the substrate protein, thus completing the reaction		GN OrderedLocusNames=PMM1287;	
CC cycle. Several rounds of ATP-dependent interactions between dnaJ,		OS Prochlorococcus marinus subsp. <i>pastoris</i> (strain CCMP 1378 / MED4).	
CC dnaK and grpE are required for fully efficient folding. Also		OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcus.	
CC involved, together with dnaK and grpE, in the DNA replication of		OC Prochlorococcus.	
CC plasmids through activation of initiation proteins (By		OX NCBI_TaxID=59919;	
CC similarity)		RN [1] NCBI_TaxID=59919;	
CC SUBUNIT: Homodimer (By similarity).		RP NUCLEOTIDE SEQUENCE.	
CC SUBCELLULAR LOCATION: Cytoplasmic (By similarity).		RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;	
CC DOMAIN: The J domain is necessary and sufficient to stimulate dnaK		RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,	
CC ATPase activity. Zinc center 1 plays an important role in the		RA Abilgarn N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell M.B., Post A.F., Regala W., Shah M., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.,	
CC autonomous, dnaK-independent chaperone activity of dnaJ. Zinc		RA "Genome divergence in two Prochlorococcus ecotypes reflects oceanic	
CC center 2 is essential for interaction with dnaK and for dnaJ		RT niche differentiation.", Nature 424:1042-1047 (2003).	
CC activity (By similarity).		RL EMBL; BX522993; CAB19746.1; -; Genomic DNA.	
CC EMBL; BA000309; BAC0309.1; -; Genomic DNA.		DR GO; GO:0031072; F:heat shock protein binding; IEA.	
DR GO; GO:0051072; F:heat shock protein binding; IEA.		DR GO; GO:0051082; F:unfolded protein binding; IEA.	
DR GO; GO:0051082; F:unfolded protein binding; IEA.		DR GO; GO:0051082; F:protein binding; IEA.	
DR GO; GO:0006457; P:DNA replication; IEA.		DR GO; GO:0006457; P:heat shock protein binding; IEA.	
DR GO; GO:0006486; P:protein folding; IEA.		DR GO; GO:0006486; P:unfolded protein folding; IEA.	
DR InterPro; IPR001623 DnaJ_N.		DR GO; GO:0006486; P:protein binding; IEA.	
DR InterPro; IPR001623 DnaJ_N.		DR SMART; SMD0226; DnaJ; 1.	
DR PROSITE; PS00076; DnaJ; 1.		DR PROSITE; PS00076; DnaJ; 2.	
DR Chaperone; Complete proteome; DNA replication; Heat shock.		DR PROSITE; PS00076; DnaJ; 2.	
SQ SEQUENCE 673 AA; 34276E46BBCB83A CRC64;		DR PROSITE; PS00076; DnaJ; 2.	
Query Match 10.4%; Score 423; DB 2; Length 673;		DR PROSITE; PS00076; DnaJ; 2.	
Best Local Similarity 25.4%; Pred. No. 3.8e-18;		DR PROSITE; PS00076; DnaJ; 2.	
Matches 191; Conservative 105; Mismatches 307; Indels 150; Gaps 28;		DR PROSITE; PS00076; DnaJ; 2.	
Qy 86 IPIDFYQVLTGAQTHFLTDGIRRAFAEARVSKPQFGESDDALISRQILQAETLSNPR 145		DR PROSITE; PS00076; DnaJ; 2.	
Db 3 IPIDFYQVLTGAQTHFLTDGIRRAFAEARVSKPQFGESDDALISRQILQAETLSNPR 145		DR PROSITE; PS00076; DnaJ; 2.	
Qy 146 RBEYNE-----GLLDEEATVITDWDKVPGALCVIQEGEGETEITVLRGEFL 194		DR PROSITE; PS00076; DnaJ; 2.	
Db 63 RDAYDRHCRTVDPDDLIAQLDPAATPHIE5DEQUSGALLLYELGNYAQVQVNLDGFL 122		DR PROSITE; PS00076; DnaJ; 2.	

DR InterPro; IPR001623; DnaJ_N.
 DR Pfam; PF00226; DnaJ; 1.
 KW SMART; SM00271; DnaJ; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 702 AA; 9938 MW; 325A8F3BE74E55BF CRC64;

Query Match	8.5%	Score 344.5	DB 2	Length 702
Best Local Similarity	20.5%	Pred. No. 4.1e-13		
Matches 161; Conservative 155; Mismatches 305; Indels 163; Gaps 31;				
Qy 86 IPIDFYQVLAQTHFLTDGIRRAFEARYSKPQFGSDIDALISRRQILQACETLSNPR 145 3 LPDHFRLIGVPSATSERILRAFQLRDKTPDEGFTEVLTORSSELRLTADLTDSS 62				
Qy 146 RREYNNEGILDDEFATVITDVPWDVKPGALCIVLQEGGETEIVLVRGEALK---ERLPKS 201 Db 63 RRDYENLILNGASS--LDLSSNREAVGLLILWESGSKEAFKIKTRKALQPOTPALGSS 119				
Qy 202 PKDVLVMLAFLDVSDA--MALDPDFITGYEFVBALKLQEBEASLAPDILRAQI 259 Db 120 READLTLLAAL---TSRDAIAEQDQRSYSNAADPLOEGIQULQRMGKLG---ELAKTL 172				
Qy 260 DETLEETTPRYVLELGLPLGDDYAAKRLNLGSGVRNLWSYCGGASALVGELTR-E-K 317 Db 173 EEDLVSLPYRIDLSSLDLNDYDSHKK---GUSMLENLKRKG---LEGKNKSETND 225				
Qy 318 FNN---BAFLR---MTAAEQVDLFVATPSNIPASPEVVEYEVALLVAQAFIGKPKHL 368 Db 226 FLNQQEFPESFQOIKPFLTVQDQLPFLQELKRGSSSEA-GFLAFLSITAIFARRXPAK 283				
Qy 369 LQDADKOFQLOQAKVNAME---IPAMLYDTRNNWEIDFGLERGLCALLGRVDECRMW 424 Db 284 JPFARKLKLNLSGLDSMPFLIGCLDLIAAD---VEQSSARPLOSSSDEKLRDW 333				
Qy 425 LGILDSESDQYRNPAIVEFVLNESENDDDDPLGLCKULETTLAGVYPERFRDTDKKFKL 484 Db 334 L-----NNYPCGEKLEAICIFCKNWLENDVLYGYRDLKBDL 371				
Qy 485 GDYYDDPMVLSYLERYVVOGSPLAAATMARIAGHAYKASAMQALQKVPSRYTDNSA 544 Db 372 DSWFEDREIQEPFIEQIE----KKSNRRTVFKSGPON-----RPIFIQAEQSLKDSS 416				
Qy 545 EPKDVQETVFSYD-PVGNVNVRGDG---EPGVFIABAVRPSSENFTDYAAGRVSSESS 598 Db 417 TGPDLNSDNFEEGRPLPQGGVREDQEVIEENYTDLBIK-NKSIETYKYALEK-IAE-- 472				
Qy 599 VDETTVEMSVADMILKB-----ASVKILAAGVAGLI---SLSFQSKYFLK 639 Db 473 -----LKFVFGEALNTTRIFKNSYLTLYAFLILFAFLGQGVFNRLKPVQEKEIID 527				
Qy 640 SSSSFORKDMV--SSMESD----VATIGSRADDSE-----ALPRMDARTAEN 681 Db 528 NSLSINENKNVYEGLNQDDKKVLDNSKILLSDNAEKVPSGEETKTAASPLE--KIEN 585				
Qy 682 IVSKWQKCKSIAAFGPDHRIELPEVILGRMLKWIWTDRAETAQOLGLVYDYLKLSVDSV 741 Db 586 LANTWLWNSKPLAGKGBINISKIVQDDLDRKEREI-LQKG1---YNNINANJENI 641				
Qy 742 TVSADGTRALIVATELBBESACSLDVHPE-----NNATDVRRTYTRBVFWSKSGW 791 Db 642 -----VLTQTAISRISVYSDLKYESEKILKIDGELINETTFTPFLKVKVTLGFSNNSW 693				
Qy 792 KITE 795 Db 694 KLVD 697				

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OM protein - protein search, using sw model

Run on: December 4, 2005, 12:39:46 ; Search time 44 Seconds

(without alignments)
1751.582 Million cell updates/sec

Title: US-10-600-070B-2

Perfect score: 4063

Sequence: 1 MEALSHVGIGLSPFQLCRLP.....YEVFWSKSGWIKITEGSVLAS 801

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR_80:*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	497	12.2	798	2	AD2144		hypothetical protein
2	429	10.6	714	2	S7082		hypothetical protein
3	145	3.6	2297	2	AB2494		hypothetical protein
4	143	3.5	2089	1	A48757		acetyl-CoA carboxy
5	139.5	3.4	879	2	JC4286		DNA-directed DNA p
6	138	3.4	2021	2	AB4771		similar to ch-TOG
7	131.5	3.2	1194	1	DJB528		DNA-directed DNA p
8	131.5	3.2	2111	2	A10668		myocerosate synth
9	130.5	3.2	1026	2	C97783		cell surface antigen
10	129.5	3.2	2110	2	B41110		myocerosate synth
11	129	3.2	1275	2	T43362		hypothetical protein
12	128.5	3.2	836	2	T30312		pilin biosynthetic
13	128.5	3.2	876	2	S70368		DNA polymerase I -
14	127.5	3.1	2472	2	E83594		still frameshift p
15	126.5	3.1	1018	2	T30853		antigenic heat-sha
16	125.5	3.1	718	2	AB1122		hypothetical protein
17	125.5	3.1	4385	2	T23042		hypothetical protein
18	123.5	3.0	673	2	C83080		probable chemotaxi
19	123.5	3.0	848	2	C70834		probable endopepti
20	123	3.0	3421	1	WB2BB6		367K tegument prot
21	122.5	3.0	899	2	HW87513		hypothetical protein
22	122.5	3.0	2756	2	T30183		hypothetical protein
23	121	3.0	1381	2	AB21010		regulatory protein
24	120	3.0	1252	2	D22122		RNA polymerase bet
25	120	3.0	1262	2	F81548		DNA-directed RNA p
26	120	3.0	3938	2	T22761		Bassoon protein -
27	119.5	2.9	692	2	G87415		glycyl-tRNA synth
28	119.5	2.9	698	2	A2593		hypothetical protein
29	119.5	2.9	831	2	S26675		DNA-directed DNA p

RESULT 1

AD2144

hypothetical protein al12707 [imported]

PCC 7120

C;Species: Nostoc sp.

strain PCC

7120

C;Note: Nostoc sp.

strain

PCC

7120

C;Date: 14-Dec-2001

#sequence_change

09-Jul-2004

C;Accession: AD2144

R.Kaneko,

T., Nakamura,

Y.; Wolk,

C.P.; Kuritz,

T.; Sasamoto,

S.; Watanabe,

A.;

Iriguchi,

Nakazaki,

N.; Shimpo,

S.; Sugimoto,

M.; Takazawa,

M.; Yasuda,

M.; Tabata,

S.

DNA Res.

8, 205-213,

2001

A;Title: Complete

Genomic

Sequence

of the

Filamentous

Nitrogen-fixing

Cyanobacterium

Anat

A;Reference number: AB1807;

MUID:2159385;

PMID:11759440

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: UNIPROT:Q8YTL0; UNIPARC:UPI00000CE525; GB:BA000019; PIDN:BAB74406_1; A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: al12707

C;Superfamily: Nostoc sp.

hypothetical protein all12707; dnaJ amino-terminal homology

%

%

%

Query	Match	Score	Length	DB	No.	Best Local Similarity	Score	DB	No.	Matches	Conservative	Mismatches	Indels	Gaps	3.9e-24
Qy	84	VPIPDYVOLGTHFTLDGIRAFEARVKSKPPQFGSSDDALISRQLQACETLSNP	143	Db	11	VRIPLDYTRILGLPLASADEQRLQAYSDRVQLPRREYSQAAIASRKQOLIEEAYVVLSDP	70								
Qy	144	RSIREY-----NEGLIJDEEAATVTDYWDKVQGALCV	176	Db	71	KERSSYDQLYLAHYDPDNAATTAKVAVENRGDSNNNGHFPDVQLSLS	128								
Qy	177	LQGGGETEVLRGEALI-----KERLPKSF-----KODVVLYMALAFDVSR	219	Db	129	LQEIGEYEVLLKGRLNQNTASTRNGNHRTPEFLDSSERPDILTVALSLELGR	188								
Qy	220	D-----ANALDPPDFITGYBFVFBEEALKLQEGEAGSSLAPDLRAQDETLEBITPR	269	Db	234	RILELLALP-QERTIBHQGLDLQSIDDRGIDGTNDQSGUNIDDLRFQQLRHH	291								
Qy	189	EQWQQGHYENASLLE-----TGQE-----VLFSEG--IPFSVQAETQADLYKLRPY	233	Db	270	YVLELLGIPLGDDYAAKRNLNGSGCVRNLLWVSGG-GGASALVGITRE--KFKENEAFLR	325								
Qy	326	MTAEQDLPFATPSNIAESPEVYEVALLVAQAFGKPKHILQDAKOFQQLQAKYM	385	Db	292	LTVABQHLFLFDG-BSKRKS-AVATYLAYAATARGFTQRQPLALTRAKQILMRSKRQ-	347								
Qy	386	AMIPAMLYDTRNNWEDEGLERGLALLIGKVDECRMWLGLODSESDQRNPAIVEFVLE	445	Db	293	AMIPAMLYDTRNNWEDEGLERGLALLIGKVDECRMWLGLODSESDQRNPAIVEFVLE	445								

ALIGNMENTS

Db	348 -----DVLHQSLCALLGCTEATRVLBSQE---YEIALI---R 383	Db	123 PNPAGGGLPQDYLISVILAHWELSREPWQQQ-----YFAATASLKALARLQQNDNDFP 176
Qy	446 MSNRDDNDLDPOLCKLLETTWLAGVVPRFRDITKDKFCKFLGIVYDDPMVLSJERV---- 500	Qy	254 DLRQIDETLEBTPRVYLELLGLP-LGDDYAAKRLNGLSGVNLWLSVGG-GASALVG 311
Db	384 EKSQDSPLLPSCLYAEQWLQNEVPHFRDLRSRQASLKDYPANQVOAQLAEALPNDAE 443	Db	177 ALEAEIROBLRPRYRILLEAKEGQSEE--QROQGALLQAMVQDRGGIEKGKEDYS 233
Qy	501 -----EVYQGSPPLAAATM---IGAEH----- 540	Qy	312 GLTRE-----KFMNEAFLRMATAEQLFLFATPSNIPAESPEVYELVALVAQAFIGKPHL 368
Db	444 TTNEAWVINRQSFSQPRGNSISGGTPVAKRPVGRNPKGEASTRTPVQRSHSEVNRFTH 503	Db	224 GLONDDFLKPIQRLCHITVAQNALFL--PESRSPSLVASYLAHVSLMAEGVKEQDPM 291
Qy	541 RNSAEPKDVQETVFSVDPGVNNVRGDCE----PGVFAIAEVPSNFETND 587	Qy	369 LQADQKFOQLQOAKVMAMEIPAMLYDTRNNWEIDFLGLERGLCALLIGKVDECRLMWGLD 428
Db	504 QNRTPDELPETSNRHRPESNSFTTARENIISTDAYTDNYPEIPEVARSR----- 555	Db	292 IVEAKSLLTIOLENCO-----DIALEKVICBELLGOTEV--VLAIAID 330
Qy	588 VAIRAGVS--ESSVDETTV----- 556	Qy	429 SEDSQYRNPAIVEFLVLENSNRDDNDLGLCKLKLLETWAGVVPFRDTKDKFPLKGDYY 488
Db	556 -VQPGSYGTOSTPQRQTPKRRRKPKQAIVNARGHSIHQQRQPSSTLGKTRLWLV 613	Db	331 QGD-----PKVIA-GLESKLATEDPPTAFAFYTFTEQWOLLEETIVPYFRDLSPETLSPKAYF 384
Qy	623 GVAIGHLSLF----SOKY-FLKs----SSSFORKDMVSSMSDSDATGSRADDSEALPR 673	Qy	489 4DPMVLSYLERVEVQ-----GSP-LAAAATMARIAGEHVKASAM-QALQVFPSPRYT 539
Db	614 G-SLGGLLFWLIVLSTFGWLNKNEFPAPSQGEQUSIQISQPLETPDKNAQIQSPPEVS 672	Db	345 NHPSVQYQLEQLEPDSDFTDNASFAPALLSTATESETPMVHSSALPDPPLTSTVPS--- 441
Qy	674 MDARTAENIVSKWQIKSLAFLGPDHRIEMLKPVDGRMLKWTDRAAETAQIQLGVYDYL 733	Qy	540 DRNSAEPKDVQETVFSVDPGVNNVRGDGEPPGVFTAIAEVPSNFETNDYAIRA----- 592
Db	673 ITEEATARKIENIWLATASALGAEHKSESLEILTGSALSQWRLIAQLQDAKDRNREYS- 731	Db	442 -RGRSPRSRSDDVFP-----SADNSSGLAVT-TLSPLAIYDTHSIGTNGIGGDS 491
Qy	734 IKLISDVSUTVS-ADGTRALVATEBLEBACSLDLVH--PENNATDVTYTTEVFWSKSG 790	Qy	593 -GVSSESSVDETTB-MSVADMLKBEASTV-----ILAAAGVAIGLISLFSQK----- 635
Db	732 HSVKVDISKSDDIDPNRASVGATRE--LTQFYENQKGSSDER-LRVYELIRQDDI 787	Db	492 NGFSSNSNAPESTSKHKSPRRRKCRVTKIRPVRFGLFLCLAGTIVGATALLINTQDPLGG 551
Qy	-791 WKI 793 -	Qy	-636 -----YFLKSSSSFSFKDMVSSMSEVATGSRADDSEALPFRMARTAENTVSKWQK 688
Db	788 WKI 790	Db	552 LLBDPLDVF-----DQPBPFIPIDEATSNLILSO---PNFNOQVGQMIVQGWLD 598
Qy	S76082 hypothetical protein - Synechocystis sp. (strain PCC 6803)	Qy	689 IKSIAFGPDHRIEMLPBYLDGRMLKWTDRAAETAQIQLGVYDYLKLKLSVDSVTVS-ADG 747
C;Species: Synechocystis sp.	C;Accession: S76082 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004	Db	599 SKCLAFGQNYDVGALQSVTLAPNLIAQQRGR-AQDQAQRVYHOYEHLQOLAYQVNQDP 657
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, Y.; Miyajima, N./o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yisuda DNA Res. 3, 109-136, 1996	R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S. DNA Res. 8, 205-213, 2001	Qy	748 TRALVEATLLESACSLDLYHPENNATDVR-TYTRYEVFWSKCWMKITEGSVL 799
A;Variety: S76083	A;Cross-references: UNIPROT:Q55559; UNIPARC:UPI00000C1133; EMBL:D63999; GB:AB001339; NID	Db	658 NRATVTARVEEISQPFILGNQQQKGSAKTDLTVRYQLVRHGWKIDQIQVV 710
C;Accession: S76082 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004	C;Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium Anal	RESULT 3 AB494	A;Reference number: AB1807; PMID:21595285; PMID:11759840
A;Start codon: GTG	A;Start codon: GTG	A;Accession: AB2494	A;Accession: AB2494
C;Superfamily: Nostoc sp. hypothetical protein ali12707; dnaJ amino-terminal homology	C;Superfamily: Nostoc sp. hypothetical protein ali12707; dnaJ amino-terminal homology	A;Molecule type: DNA	A;Molecule type: DNA
F;6-70/Domain: dnaJ amino-terminal homology <DNJ>	F;6-70/Domain: dnaJ amino-terminal homology <DNJ>	A;Residues: 1-2297 <XUR>	A;Residues: 1-2297 <XUR>
Query Match 10.6%; Score 429; DB 2; Length 714;	Query Match 3.6%; Score 145; DB 2; Length 2297;	A;Cross-references: UNIPROT:Q8YI08; UNIPARC:UPI00000CEEDD; GB:BA000020; PIDN:BAB78214.1;	A;Cross-references: UNIPROT:Q8YI08; UNIPARC:UPI00000CEEDD; GB:BA000020; PIDN:BAB78214.1;
Best Local Similarity 25.1%; Pred. No. 8 5e-20; Matches 194; Conservative 124; Mismatches 331; Indels 124; Gaps 30;	Best Local Similarity 19.6%; Pred. No. 1.4%; Mismatches 273; Indels 170; Gaps 29; Matches 136; Conservative 114; Mismatches 114; Indels 273; Gaps 29;	A;Experimental source: strain PCC 7120	A;Experimental source: strain PCC 7120
Qy	86 IPIIDFQVYGAQTHFLTGIRAAFEAVSKPQGFGRDADLTSRQOLQACETLSNPRS 145	Qy	89 DFTQVLAQTHFLTDGGRRAFEARSKPQFQGSDDALISRSRQOLQACETLSNPRS 148
Db	3 IPIIDFYLGIIPQSGGATIEQYDQLQPLREFDAAUTLQRNLQIAVETLDRPEK 62	Db	273 EFTQIKGIAAT-----IAPHVNEP-----RRREILKCALDLVRKTRGSTD 311
Qy	146 REYNE--GLDDE-EATVITDVPDKVP---GALCVLQEGGETEIVRGEALLE 196	Qy	197 RLPKS--FKQDQVWLMALAFDVSRDAMALDPDFITGYEFVBEA-LKLOQEGASSLAP 253

Qy	149 YNE-----GLDDDEATVITDVPPWDVKPGCALCVLQEGETEIVIRVGELLKER 197	Qy	73 LPPSITDRPERHVPPIPDPYQVLGAOTHPLTDGIRRPEARVSKPP-----QFGFDDAL 126
Db	312 FISVENITSLSINLAALDDEERTSYFQQAELPEKI----ENGVN- -IFSIIAQLTFF 365	Db	197 LPNALIK-----LGKFKIGPTGPVMSVLGKIAANILAQAKVPSIPWSSGFGGDGP 250
Qy	198 LPKSFQDVTLVMAFLDVSRAALDLP-----DFITGEFYBEALKLQOEE----G 247	Qy	127 ISRROQILOAACETLNSPRSRREYNEGILD--DDEATVITIDPWFWDKVPGALCVLQEGG--- 181
Db	366 EPOLEKLTIEIVNNLERGDIQREALVAIAPYLKPSEPIIQLQALEIAKYKANEYDRIKA 425	Db	251 LQ-----ADLTEBTIPEIFNKGLVTSADEAVINKIGWE -GIMIKASEGGKK 301
Qy	248 ASSLADPLRQ-----IDETLBETTPRYVLELLGLPLGDDYAAKRNLNGLSEYRNILW 299	Qy	182 -----ETEIVLR-----VGEALLKERLPKPKQDVYUVMALAFDYSRDAMALDP 226
Db	426 LAATAPHLKETOCNEBVLYLIERLENINIFI-----SCVSETLV 465	Db	302 GIRFTDNEADLRNAFQVSNEVIGSIFLMOQCLKNRHIEQVIG---DQHGNVALNG 357
Qy	300 SVGGAGASLVLGGT TREKPMNEAFLRMTAEQVLDLFPATPSNIPAE-SPEVVEYALALVA 358	Qy	227 PDFITTYEFVVEALKLQKQECASSLAPLDLRAQIDEATEBTPRYVTEBLGLPLGDDYAAK 286
Db	466 FI----ASVL--SKSQSKLQKAF-----EIPAMLYDTRNWEI 402	Db	358 RDCSIIORRF-----OKIFEBGPPSTWP-----KETFHFM-----ELAAQ 391
Qy	359 QA-PIGK-KPHLJQADKOFQQLQO--AKVAMM-----EIPAMLYDTRNWEI 402	Qy	287 RLNGLGSVRNTLWSVCGGASALVCGCLTREXKFMNEAFLRMTAEOYDLFVVA--TPSNIP 343
Db	503 LAPHLSKLEPQLQOALKTAINKEGASKVVALPAVIPHLPQSKSQLLKEFETIQTEY 562	Db	392 RL-----TONIGYQ-GAGTVEYLNAADNKF-----FLENPRQVHPVPTBGTGANLP 441
Qy	403 DFGHLERGLCAL-----LIGKVDECWMIGLDSESDSOYR- -NPAl 439	Qy	344 AES-----PEVYEVALALVAQAFIGKPHLJQADKOFQQLQOAKYKAMEIPIA--- 391
Db	563 DNARSRALVALVPHLSDFSHLIDSLEIIEKLVSTYOSKA-QALVAVAPOLRKFNSSL 621	Db	442 ATOLQVAMGIPLFNPDIRRLYGRDAYGTDP--IDFLQRYREL_DSHVIAARTAEPN 498
Qy	440 VEFYLE---NSNRDDNDLDPGLC-----KLIETWLAVGIVFPFRDTDKKFUKGD 486	Qy	392 -----MLYDTRNNW-BIDFGJBERGLCALLIGKVDECWMIGLDSESDSOY--- 434
Db	622 LQKALEIAKKINSDEQKDEALAAIAYQOLSESEPELLEYQKLIAQNTYTHSHHKHRJALIP 681	Db	499 DEGKPKTSIERIKFOSTPNWGVGFPSVGANGGI-----HEPADSOFGH 542
Qy	487 YYDPPMVLSYLERVEVQGSPLAAAATMARIAGAEHVKRASAMO- ALQKYPEPSRYTDRNSAE 545	Qy	435 ---RNP-----AIEVPLVLENSRND-NDLPLGICLKLET-----WLAGVVFP 472
Db	662 YLREPQQTBFQLYFSATASLASAAPL-- -PEPKRSSEVQEAQMLDUDANTSDLIRAN 738	Db	543 LFARKSPNREQARKALVALKEMEVGRDIDNSVEYLWKLRLTEAFAKNTIDTSWLDGII-- 600
Qy	546 PKQVQETVFSVPDVPGNNVGRDGPGRGVTAIAEAVRPSENSETNDYAIRAGYSESSVDETY- 604	Qy	473 RFRDTKDKEPKLGDYYDDPMVLSYLERVETWQGSPLAAAATMARIAGAEHVKRASAMQA--- 529
Db	739 ELKIVPLIISKT-----EOKERKVIETAKTIK- NDTPKGAEELAYAVENTHLSBFDQVKIF 790	Db	601 -----KEKSVKV-----EMPSHL---VYVGAAVFKAPEHVVKVATEEYKESFRGQVS 644
Qy	605 EMSVADMFK---EASVKLILAGVAGILSLFSOKYFLKSSSSPKQDMVSIMPSDSVATIG 661	Qy	530 -----LQKVFSRSTYDTRNSAEPKDQYT----- 552
Db	791 FLETERLKAIENDSSKAKALAVVPIYLSKSSPSBSLDKAFPEIAENLYQOSQCQFPDDLVLA 850	Db	645 TAGIPGINSNTEVAYLDTKYPFVERBISDVYRFTLDGNTIDVETVOTAEGLALLFGG 704
Qy	662 S-YRADDSSEAIPMDARTAENTVSKWQOKIKSLA 693	Qy	553 ---VFSVD-PVGNNNVGRDGE---PGVFTAEARVPS-----ENFETNDYAIRAGYSES 597
Db	851 THLKERECIJKLLEQALEKARDIDSEYQOAQDFA 883	Db	705 ETRHIFGMDEPLGLRLSLDEATVLMPTIFDSELTDVGKXVRYLQDNGATVEAG--- 760
Qy	883	Qy	598 SVDETTVENSVADMILKEASYSKILLAGVAIGLISLSQKYPLKSSSSQFQDMVSSME-SD 656
Db		Db	761 ---QPYVEYEAKMNI-MPIKATESGG-----KITHNLSAGSVISAGDILLASJELKD 806
Qy		Qy	657 VATIGSV----RADDESEALPRMDARTA-ENIVSKWQKIKSLAFGPDHRIEMPLPEYLDGR 710
Db		Db	807 PSRVKKIETFSKGKLDIMESKVLDLFEQKAVMNVL-----GFNLID---PEVAQQ 852
R; Roessler, P.G.; Ohriroge, J.B.		Qy	711 MLKJWTDRAETAOLQGLYXD-YTLLKLSYDSDVTVTSAQDGTRALVATEEESACLSLIVHPE 769
J. Biol. Chem. 268, 19254-19259, 1993		Db	853 AIDSATSSAADDLIVQVLDEFYRVEQSQFDGV-IADDVVRLTRKANTE---TLDVVIS 907
A; Title: Cloning and characterization of the gene that encodes acetyl-coenzyme A carboxylase		Qy	770 NNA 772
A; Reference: A48757; PMID:8103514		Db	908 NLA 910
A; Status: preliminary; nucleic acid sequence not shown		Qy	RESULT 5
C; Genetics:		Qy	JC286
A; Introns: 25/1; 729/1		Qy	DNA-directed DNA polymerase (EC 2.7.7.7) - Bacillus stearothermophilus
C; Superfamily: human acetyl-CoA carboxylase	- Cyclotella cryptica	C; Species: Bacillus stearothermophilus	N; Alternate names: DNA polymerase I
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004		C; Date: 14-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 17-Mar-1999	C; Accession: JC4286
C; Accession: A48757		R; Zhang, S.M.; Teo, C.Y.; Lo, E.; Wong, V.W.T.	A; Title: Cloning and complete sequence of the DNA polymerase-encoding gene (BstpolI) and
R; Roessler, P.G.; Ohriroge, J.B.		Gene 163, 65-68, 1995	A; Reference number: JCA4286; PMID:96001245; MUID:7557480
J. Biol. Chem. 268, 19254-19259, 1993		Best Local Similarity 20.0%; Pred. No. 1.7;	A; Accession: JC4286
A; Cross-references: UNIPROT:Q39478; UNIPARC:UPI00000A5A26; GB:L20784; NID:91065903; PIDN		Mismatches 113; Mismatches 289; Indels 272; Gaps 44;	

A: Molecule type: DNA
 A: Residues: 1-879 <RHA>
 A: Cross-references: UNIPARC:UPI00001757A1; GB:U23149
 A: Note: The authors translated the codon GCG for residue 15 as Arg
 C: Comment: It has three enzymatic functions: 5'-3' exonuclease activity, DNA synthesis and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 C: Genetics:
 C: Gene: Bstpol I
 C: Superfamily: DNA-directed DNA polymerase I
 C: Keywords: nucleotidyltransferase

Query Match Score 139.5; DB 2; Length 879;
 Best Local Similarity 22.0%; Pred. No. 0.71; Mismatches 315; Indels 173; Gaps 44;
 Matches 175; Conservative 132; A:Accession number: A84420; MUTD:10617197
 Qy 99 HFLTDGIRRAFEARVSKPQQFGFDDALISRRQILQQAETLSNPRSRREY-NEGILDE 157
 Db 108 HYEADDLIGTMAAFAARE--GFPAVKVLSGRDLTQ---LASPOVTVETTKGTIDIE 159
 Qy 158 EATVITDV-----PMDKVP-----ALCVLQGGEPBIVLRVG 190
 Db 160 SYTPETVVEKYGLTPEQIVDLKGMLGDKSDNI PGVPGIGKKTAVKLXQGTVENVLASI 219
 Qy 191 EALLKERLPKSFQ--DVIYVLMALAFDVSRA--MALDPDPFITGYEFVERBALKLUQE 245
 Db 220 DEIKGEKLUENLROYRDIAL-LSQQLAAICRDAAVELTID--DIVYKGDBREKVVALFQE 276
 Qy 246 EGASSLAPDRLRAQIDE-----TLEETPTRYVLELGL--PIGDYIAKRLNG-
 Db 277 LGFQSFLDKMAYQDDEGPXPLAGMDFAATSVTDEMADKAALAVVVEGDNYHAPIVGI 336
 Qy 291 -LGSVNRNLM-----SVEGGASALVGGTREKEM-----NEAFLRMTAAEQV-D 333
 Db 337 ALANERGRPFRLRPTETAVADPKFLAWLGEDTKEKTMFDSSKRAAVALNGKIGELAGVVFDF 396
 Qy 334 LEVATPSNIPAES-----FEVYEVALLAVAOAFIGK-KPHLQLDADKQFOQL--QOAK 383
 Db 397 LLLAYLILDPDAQAGDVAAVKMHQYEAVRSDAEVYGRGAKRVTVPDDEPTLAOLVRKAAA 456
 Qy 384 VMAMEIPAMLYDPTNNW-1DFGLERGLCALLIG-----KVIDECRM-WLGLD-SEDSQY 434
 Db 457 IWALEPLMDELRNNEQDRLLTEHALAGLILANMEFTGVKDVTKRLQMGAALETEQQL-
 Qy 435 RNPVIAEFTLVENSNRDDNDLPGKCLLTLWLAGVVFPRERDTDKKCFKLGDYDDPMVL 494
 Db 516 --AVERRYYELAQEFINISP---KQLT---VLFEDKLQLPVLKTKTGT-YSTSADV 564
 Qy 495 SYL-ERVEVYQGSPAAAATMARIAGAHTHKASAMOALQKVFPSRTYDNRSAEPKDQET- 552
 Db 565 EKCLAPHHEITVE--HILHYTQLQGLQSTYIE-GILJKVHHTVGTQVHTMPNA---LTTG 617
 Qy 553 -VFSYDPPVGNVNGRDPGEQPGVFIARVRISE-----NFETNDYAIRAGVSESSVDETT 603
 Db 618 RLSSYEPVNQNPITRLEEGRKIRQAFVPLFAADYSQIETLRLVIAHAB--DDNL 674
 Qy 604 VE-----MSVADMILK8-----ASVKILLAGVATGIGLISLFSQKFYFLSSSFORK 647
 Db 675 IEAFRWLDIHTKTAAMDIFVSEEDVTANRROQAKAVNFGIVYGISD-YGLAQNLTTRK 733
 Qy 648 DMVSSMESDVATIGSVRADDSSEALPRMDARTAENIVSKWQKIKSLAFGPDHIREMLPEVL 707
 Db 734 EAEEFTERYFASFPGVK-----QYMDNTIVQOE-AKOKGYVTTLHRRYLPDT 780
 Qy 708 DGRM-LKIWTDRAA-ETAQIGLIVYDVTLLKLSVD-SVTVSADGTRA-----LVEA 754
 Db 781 SRNFNVRTPAERTAMNTPIQGSAAD-IIKKAMIDLSSVTEERQARLILQGHDELLEA 839
 Qy 755 TLEESACLSPLVHP 769
 Db 840 PKEETGRCLCLV-PE 853
 Qy 860 ITPMLLGKGFESPDWTKMRL---ESIE-----AVNKILBEANRKTQPTGTG---ELFGG 905
 Qy 635 KYFLKXSSSFQRKDMVSSMESDVATIGSVRADDSSEALPRMDARTAENIV-----SKWQK 688

similar to ch-TG protein from Homo sapiens [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 R:Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Ni, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tillon, L.; Eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Accession number: A84420; MUTD:20083487; PMID:10617197
 A:Status: preliminary
 A:Cross-references: UNIPROT:Q9ZQN6; UNIPARC:UPI000017A6E6; GB:AE002093; NID:G4263790; PII
 A:Gene: At2g15630
 A:Map Position: 2

Query Match Score 138; DB 2; Length 2021;
 Best Local Similarity 20.2%; Prd. No. 3.3.; Indels 272; Gaps 43;
 Matches 179; Conservative 122; Mismatches 315; Prd. No. 3.3.; Length 2021;
 Query Match Score 138; DB 2; Length 2021;
 Best Local Similarity 20.2%; Prd. No. 3.3.; Indels 272; Gaps 43;

Qy 39 ASKADRLLSDENFTSDSSSSPATATTATLVSLLPSIDRPERHVPIDFYQVLLGAQT 98
 Db 297 ATKWSERKEAVASLTKLASTKLAPGDFSEICRTLKLII-TDVNLAVAVEALQAGIN-- 352
 Qy 99 HFUDGJTRAFEARVSKPQFQGFSDDALTSRQLQACETSNPRSBREYNEGLDDDE 158
 Db 353 -LACGLRTHFSA-----SSRMFLPVILLEKL----KEKKSQVTDPLT 388
 Qy 159 ATVITYDVPWDKVPGALCIVLQEGGETEVILRVGEALLIKERLPLKSFKDQYVLYMA---LA 213
 Db 389 QTQIQT-----MYKAG---CLNLYVIEGRNVKTAVKNKPVLVRSTLTWLT 431
 Qy 214 F-LDVSRDAMALDPPDFITGYEVTEALKLQFEGASSLAPDLR-----AQID- 260
 Db 432 FCLETNSKALIK-----AHKEYVPLMCELNQG-----TPDVRDAAFSALAALAKSVM 481
 Qy 261 -----ETLEBTPTRYVIELLGPGLDDYAAKRLNGLJSGVNLWSSVGGASALVGGL 313
 Db 482 RPLERSLKEKDDVVKKKLSEMIAGSGGDQA-----GTSVV-TVQSVGSTARGCLHNRY 535
 Qy 314 TREKFM--NEAFLRMTAAE-----OVDLFVAT-----PSNI 342
 Db 536 TTSEPMQNSDASPVRSKASMSLGSKRPAFSAQSKKVTGKPSGKRDGSVRNEGSRSVE 595
 Qy 343 PAESFPEVVEALLVQAQFIGK-KPHLQLDADKQFQ--QLOQQAQVAMMTEPAMLYDTRN 398
 Db 596 PPEDEVPAEMGLEEINR-LGSLVKPTVSQLSSWVCRLEATLAKBEIEGL--- 648
 Qy 399 NWEDFGLR---RGLCALLJIGVDECHRWLGLODSESOYRNPAIVEFLEN--SNRDD- 451
 Db 649 -QELDKSVEILVRLCAV-----PGNNEKNVQL-----FSFENYFFSNLPDF 689
 Qy 452 -----NDLPLGSLCKLLETLWLAGVVFPRFRDTDKKCFKLGDYDDPMVL 494
 Db 690 SINSLGTSERVADIKTRASAMKCUTAFCEAVGPGFVFLR-----FKIMKEHKNPKVL 742
 Qy 495 S-----YLERVEVQGSPPLAAATMARIAGAHTHKASAMOALQKVFPSRTYDNRSAEPKDQET- 521
 Db 743 SEGLLWWMVASDDDFGVSLIKLKD1DFCKDVGQLOSSSTAATRNATIKLJGALKHFVGPDIK 802
 Qy 522 -----VKSAMOALQKVFPSRTYDNRSAEPKDQETVSVDPVGNGVNRDGEPEGVFAEA 576
 Db 803 GFLNDVKPALLSALDTEY-EKNPPEGTAPKRVVKT--SVSTSTSGGLDSLSPREDISTK 859
 Qy 577 VRPS--ENFETNDYAIRAGVSESSVDETTVMSVADMILKEASVTKLAAQVAGLJLSLFSQ 634
 Db 860 ITPMLLGKGFESPDWTKMRL---ESIE-----AVNKILBEANRKTQPTGTG---ELFGG 905
 Qy 635 KYFLKXSSSFQRKDMVSSMESDVATIGSVRADDSSEALPRMDARTAENIV-----SKWQK 688

RESULT 6
 A84420

Db	906 ---LRGRLLDSNKRNLVM---QTLTTIGGYAAAMGPAVEKASKGTLSDVLLKCLGDNKHHMR	959	Qy	533 VFPSSRTYDNRSAEPKDVKQETVFSVDP-----VGNNVGRDGEPEGYFTAE--AVRPSNENFET	585			
Qy	689 IKSLA----FGPDHRIEMLPEVL---DGRM-----IKWTDRAAETAQLGLVYDT 732		Db	711 LNPSD-----ATFTVCGKRLFVRSNV-RESLGLVILKDWLAMRK----- 750				
Db	960 ECTLAALDIWLGAVHLDRKMPYIYLALTGKGAEGRKDLEFDNL---TKQTLGLSDRV 1014		Qy	586 NDYAIRAGCYSSESSVDETTVEMSVADMKEASVKILA-----AGVIAIGLIS----- 630				
Qy	733 ---LLKLSVDSTVVSADTRALVEATLBSACSLDVHPENNATDVR 776		Db	751 ---AIRARIPGSSSDE-----AVLLDKQOQAIIKVYCNVSYGGFTG/YAQGFLPCLVYVATVT 802				
Db	1015 DAIIHLKPASTMTDKSADVTKAEGCISBELLVSGQEMIEKLKDQ 1062		Qy	631 -----LFEQKYKURKSSSFQR-----KDSLAFGPDHRIEMLPEVLDGMRMLKIWTDRAAETAQLGLVYDYL 677				
RESULT 7								
DDBJ/28	DNA-directed DNA polymerase (EC 2.7.7.7) - human herpesvirus 3		Qy	678 TAENIVSKWQK-----IKSLAFIGPKHMLIISTALFCPPKILECEKTFI--KLILL-----TKKRYIGVYGGKV 915				
C;Species: human herpesvirus 3, varicella-zoster virus	C;Accession: B27214		Db	803 TIGROMLLSTRDYIHNWNAAFERFTAPPDIESSYLSQRAYEVKVIYGDTSVFLFKGV 862				
C;Species: human herpesvirus 3, varicella-zoster virus	C;Accession: B27214		Qy	863 SVEGIAKIGKRMHIIISTALFCPPKILECEKTFI--KLILL-----TKKRYIGVYGGKV 915				
R;Davidson, A.J.; Scott, J.B.	J. Gen. Virol. 67, 1757-1816, 1986		Db	734 LKLSYDSDVTVS-----ADGTRALVEATL-----EESACLS 763				
A;Title: The complete DNA sequence of varicella-zoster virus.	A;Reference number: A27345; MUID:86306657; PMID:3018124		Db	916 LMKGYDLYRKNNCQFINDYARKLVYELLYDDTVSRAAABSCVS 959				
A;Accession: B27214	A;Molecule type: DNA		RESULT 8					
A;Residues: 1-1194 <DAV>	A;Cross-references: UNIPROT:P09252; UNIPARC:UPI0000129829; EMBL:X04370; PIDN		Db	A70668 mycocerosate synthase (EC 2.3.1.111) - Mycobacterium tuberculosis				
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase	C;Species: Mycobacterium tuberculosis		Qy	C;Species: Mycobacterium tuberculosis				
C;Gene: 28	C;Accession: A70668		Db	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004				
C;Superfamily: DNA polymerase	R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.		Qy	R;Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.				
C;Keywords: DNA binding; DNA replication; nucleotidyltransferase	Nature 393, 537-544, 1998		Db	Nature 393, 537-544, 1998				
Query Match Score 3.2%; DB 1; Length 1194;	A;Authors: Squares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.		Qy	A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome				
Best Local Similarity 19.0%; Pred. No. 3, 8;	A;Reference number: A70500; MUID:98293987; PMID:9634320		Db	A;Accession: A70668				
Matches 168; Conservative 122; Mismatches 297; Indels 297; Gaps 44;	A;Status: nucleic acid sequence not shown; translation not shown		Qy	A;Molecule type: DNA				
48 SDENFTSDSS---SSFATTATATLSSLPPSITDRPERHV--PIPIFDYQVQLGAQ---TH 99	A;Residues: 1-2111 <COL>		Db	A;Cross-references: UNIPROT:P96291; UNIPARC:UPI000036BA0; GB:AU123456; NTID:9:				
205 NDATLNGDRNAAFTGTSKSPASPEFRV--IERTDVYYDTQPCAFYRYSPSSKFTN 261	C;Experimental source: strain H37Rv		Qy	C;Genetics:				
100 FLTDGIR---RAPEARISKPKPQGFSDDALIS-----RRQI-----132	C;Superfamily: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] synthase I homologe; acyltransferase; [acyl-carrier-protein] S-malonyltransferase homology		Db	C;Superfamily: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology				
262 YLCDFNFHPELKYYGRVDAFTRFLMDNPFGFVSEFGWYQLKPGYDGERYVRPAPRQLTSD 321	C;Keywords: acyltransferase; carrier protein; coenzyme A; phosphotransferase		Qy	F;27/426/Domain: 3'-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>				
133 LQAACT----ETLSNPRSRREYNEGLDDE-----EATVITDPMWDKPGALC 175	C;Gene: mab6		Db	F;54-815/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>				
322 VEIDCMSONLQALPNDDSWPDYKLLCPICXSGSNBLAFTPATHEDL---VIQISC 377	C;Superfamily: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	F;1444-1733/Domain: long-chain alcohol dehydrogenase homology <LADH>				
176 VL---QEGGETEIVLRYGEALKERLKPFSFKQ-----DVVLMVALAFDVSRD 220	C;Gene: mab6		Db	F;1765-1945/Domain: short chain alcohol dehydrogenase homology <SDADH>				
378 LLYSIPROSLEHILLFSLGSCLDLPQTQVQEMKDAGLPEPTYLEFDSRFELLIJAFTMLVHQ 437	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	F;2016-2096/Domain: acyl carrier protein homology <ACP1>				
221 AMALDPPPFITGYBFEBALKLQEAGASSLAPDLRQIDTELEITPRYBLGLPLG 280	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	Query Match Score 3.2%; Best Local Similarity 19.9%; Pred. No. 9, 4;				
438 Y---APEFAITGYNINEDWAFI-----MEKLNISIYSLKL-----468	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	Mismatches 82; Indels 289; Gaps 33;				
281 DDYAAKRANGLSEGRVNLWSVGGGASALVGGLTREKFPMNAAFLRMTAAEVQDLFVATPS 340	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	Matches 151; Conservative 82; Mismatches 237; Indels 289; Gaps 33;				
469 DGYSGSINGGLFKI---WDVGKSG-----FQRSSKVKINGLISLDMYIAIE 512	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	151 BGLDDBEATVTDVP---WDK-----VPGCALCVLQEGEGETEVIRGEALKERL 198				
341 NPAESPEVEYEA-----LALAQAFIG 363	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	29 ESLLRGDD-LVTEIPDRWDADDYDPPGFGVR-SVSRWGG-----68				
513 KUKLSSYKLDSVAREALNESKRDLPYDIPGYASGPNTTRGIGEYCIQDSALVGKLFKK 572	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	199 PKSFQDQVYLVMAFLDVSRDAMALDPDFI---TGYEFVEREALKLQEEGASSLAPDL 255				
364 KEPHLLQDADKOFQQLQOAIIKNAMEIPAMLYDTRNNWBIFSLERGLCALLIGKVDECRM 423	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	69 ---FLDVAQFDASFEGFSEREATVETGLTH 129				
573 YLPHELSA-----VARARILITKAIID-----GQQVRYTCLGLASS---612	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	256 RAQIDETLEBITPRYVLELGLPIGDDYAAKRNLGLSGVNLMSVGGGASALVGCGLTR 315				
424 WLGLDSEDPSQYRNPAIVEF-----VLENISNRDDDLFGLCKLLETWLAGV-VFPR 473	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	110 -----GLDPASL-----ASSTAVETGLTH 129				
613 -RGPILPDDGY--PATPEYKDVIPDVGDVBEEMDEDSVSPGTTSSRNVYQKGARFDF- 668	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	316 EKPNNEAFRMTAAEQDLFVATPSN-----PAESFEVY-----350				
474 PRDTDKDKFPLGSDYDDPMVNSYLERV-EVYQGSPPLAAAMARIGAEHVKASAMQALQK 532	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Db	130 EDYL---VLTTRGGLASPYVUTGLNNNSVASGRIAHTLGLHGPAMTFDTACSSGLIMAVHL 186				
669 -PDT-----GFIYDPPVVLDFASLYPSIIOQAHNL-CFPTLTLNAPETVK-----R 710	C;Keywords: mycerotic acid synthase; 3'-oxoacyl-[acyl-carrier-protein] S-malonyltransferase homology		Qy	351 -----EVNALVAQAFIGKKPHLL-----QDADKQFQQLQQAK 383				

Db	187 ACRSLHDGEAIDALAGGCAVILEPHASVAASAQGMLSSTGCHSFADADGFVRSEGMAM 246	Qy	341 NIPAESPEVVEYVALIYAQAFIGKPPHLQDADKQFQQIQQAKWMA-----MEIPAM 392
Qy	384 VNAMEI PAMLYDTRNWEIDGLLGIKVDCRMIGLCLLIGLKVDSQRNPALIVEFV 443	Db	561 KVNSELSNAEKOLLGSVLKKGVEAVQVLSPACQQLMOGHLYKIMAEOTKKDTKVKNDI 640
Db	247 VLLKRLEDALEDFGNR --- IFAVVRATATNDGRTET --- LTMPSEDAQY --- AVYRAA 295	Qy	393 LYDTRNNW-----IDFGLERGLCALLIGKVDECRMWGLDSEDSQYRNPAI 439
Qy	444 LENSDDNDLDPGLCKLLETFWLAGVYFPRFRDTKDKKKFGLGDYYDPMVSYLERYEVV 503	Db	641 LFPLPSNTELKTNTNQIAITSNVLDGPATAEVKGEBIIQATNTIAGSLEAQD --- KAAI 696
Db	296 IAAAG ----- VOBTVGIV ----- EAHGTTPIGDPIEYRLARV-YG 332	Qy	440 VEPFLEN ----- SNRDNDDIDPGLCKLLETFWLAGVYFPRFRDTKDKKKFGLGDYYDPMVSYL 497
Qy	504 QGSPLAAATMARIIGEHVKASAMOLOQTVF ----- PRYTDRNSAEPXDVQETVFS 555	Db	657 IKGVGETIATHSDTSLSLSPNKALIMASEKGIA ----- ESOTNLPD - RELMTKGLV 746
Db	333 AGTPCALGSAKSNNMGHSTASAGTVGHLIKALLSLRHGVVPPLHFNRLPDELSDV ----- 386	Qy	498 ERVEVVQGSPLAAAATMARIIGAHVKASAMOLOQV ----- FPSRYTDRN 542
Qy	556 VDPVGHNNGRIGDGEPGVFTAIEAVRPSNINFETNDYA - TRAGVESSVDTETVMSADMKE 614	Db	747 DGYEGKCGPEITKAASSGGIDNSNINDSBEKEALKRKAKDASEAALDRTDQNLTEGFKGQN 806
Db	387 ----- ETGLFVPOQVTPWN ----- GNDHTPKRVAISSEGFMGCTNVAIVEBAPF 432	Qy	543 SABPK ----- DVQETVFSVDPVGNNNGRDGEPGPVIAE ----- AVRP 579
Qy	615 ASVKILLAAGHVA-IGLISLPSQSKYFLKSSSFORKDMVSSMSDSDVATIGSVRADDSRALPR 673	Db	807 TEEHKPHDDIYNKAREVINAIVNPVIEALEKSKEPVVAASERTIVQETSSINNISKLAVER 866
Db	433 ASAPESSPGDLEVG ----- PRFLMWSSTS	Qy	550 SENFETDYAIRAGVSISSVDETTVMSADMKEASVILANGVAIGLISLFSQSKYFLK 639
Qy	674 MDARTAENIVSKWOK ----- IKSIAFQGDPHR ----- IEMPEVLDGRML 712	Db	867 VNFF ----- RAMLSPNGNLKLEEK ----- KEBAAIKKVDI --- LVKAFTGTTKSTE 908
Db	462 QTAROLATWEEHODCVAASDLAYTLARGRAHHRPVRTAVVANLPLEVGEIREVADGDAL 521	Qy	640 SSSSFORKDMVS ----- SMEVDVATIGSVRADD -- SEALPRMDARTAE - NIVSKWQKIKSL 692
Qy	713 ----- KIW- TDRAEATAQGLL ----- YDYLDTKLSSVTSVTSADGTRALV 752	Db	909 EQQSFIKTNLIDDKTLLSKBVRLQIOTIDKLLQEQRSEATEPNSVTEIDVRVSGKSLLKPI 968
Db	522 YDAVHGHDGRPVWVPSGQGQWAAMGTQLIASEPVFAATAKL --- EPVIAAESGSFVT 578	Qy	653 A 693
Qy	753 EA-TLBESACSDLVHPENNNTDVRYYTTRYFVFWPSKG 790	Db	969 S 969
Db	579 EAITAQQTVTGIDKVQPAVFFAQVALAATMECTYGVTRPG 617		
RESULT 10			
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		C:Species: Mycobacterium bovis	mycocerosate synthase (EC 2.3.1.111) - Mycobacterium bovis
		C:Accession: B44110	C:Sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
		R:Mathur, M.; Kolattukudy, P.E.	C:Cross-references: UNIPROT:Q02251; UNIPARC:UPI000012ED5D; GB: M95808; NID: G149977; PIDN:?
		R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; RC	R:Mathur, M.; Kolattukudy, P.E.
		Science 293, 2093-2098, 2001	J.Biol. Chem. 267, 19388-19395, 1992
		A>Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.	A:Note: the source is designated as Mycobacterium tuberculosis var. bovis Bacillus Calmette Guerin.
		A:Reference number: A44110; PMID:1527058	A:Reference number: A44110; PMID:92466887; PMID:1527058
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Db	378 BPPQYKQVPTPITPTQLOP - ETSQMPQS-QQVNPNLN - TATALSGSMQDLNLYVN 432	Db	29 ESLIRGDD - LYTEIPDRWDADDYDDEPGVGR - SVSRWGG ----- 68
Qy	171 PEAICLQVQEGGTEIIVRGALLKERLPKSPKQDVVLLMA - LAFIDVSDAMALDPPD 228	Qy	199 PKSFQDQVVLVMAFLDVSRAALDPPDFI --- TGYEVFEAALKLLOBEGASSLAPDL 255
Db	433 AGLTKAIDSNQOIDLKEAAAILNNNE --- KSDAAEKOANIIIALENTYNNKLPDA 487	Db	69 --- FLDDYAGFDLEFFGISEREATSIDPQRLLLETWEAIEHA --- 109
Qy	229 FITGYEYERALKLLOBEGASSLAPDLRAQI ----- DETLEBIBTPRYVLEL --- LGPLPLG 280	Qy	256 RAQIDETLEEITPRYVLELLGLPQGDYYAAKRLNGLSGVRNLWVGGGASALVGGLTR 315
Db	488 KWTGYNNAVLETIKNDONTPNJEKSKNLEATAVLNSENBLPKQKOMLXEAVIDVGSLSK 547	Db	
Qy	281 DDYAAKRLNGLSGVRNLWVGGGASALVGGLTRMNEFLRMTAASQVDFVATPS 340	Qy	
Db	548 DD - ASRAAADGIKOVY ----- IKSNLSPPEKMLTAVGD 580	Qy	

Db	110	-----GIDPASL-----AGSSTAVPGLTH 129	Db	98	LPPAD-----APLMRASIGGLE SLLAQADATQWELGTIAQIPRRAVAGLIA-----L 144			
Qy	316	BKPNNEAFLRMTAAEQVDLFLVATPSNI-----PAESFEVY ----- 350	Qy	426	GLDSEDS-----QYRNPAVLFVEVLNRSNRDDNDLPGLKCKLLETLAGVVFRFRDTKD----- 479			
Db	130	EDYL-----VLTTRAGGLASPIVVTGINNSVASSGRIAHTLGLGPAMTFDTAASSGLMVAHL 186	Db	145	ALDPKPVKRRAQBALRNLNKNPPPSFSLDHPAAMAEATANQSL-----RLYADKAQQ 199			
Qy	351	-----EVALALVAQAFIKGPKHILL-----QDAKQFQQLQQAK 383	Qy	480	-KKFKLGDYDDPMVLSYLERVEVHQ-----GSPLAAATM-----ARIGAEHVKASAM 527			
Db	187	ACRSLHDGERDLALAGGCAVILEPACVAASAQGMSSTGRCHSPDADGFLVRESEGCA M 246	Db	200	RKEKTTTDSPTDPELIALQKVAVASGGWPSSKTSLSCLCELLSIAARTGNEMHMSMAYF 259			
Qy	384	VMAETI PAMLYDTTRNNWEIDFGELGLCALLIGKLIGKEDCRAWLGLDSESDQYRNPAVLFV 443	Qy	528	QALOKVFPSPRTYDR-NSAEPKDVOETFSYSDPGVNN-----YGRDGEPGVFIAFA 576			
Db	247	VLKRLPDALDGRNR----IAVVEGTTATNQGRIBT----LTMPSEDAQV--AVYRAA 295	Db	260	EIFEMFMFGNAADEVASKUPRLLEIRELPEAPNDQQLLPPWIAISLRAYD-----VaqQ 315			
Qy	444	LENSENRRDDNDLPLGSIQKLLKETLWLAGVVFPRFRDTDKKFKLGDYDDPMVLSYLERVEV 503	Qy	577	VRPSENFE-TNDYAIRAGYSES-----SVDETTVEMSVADMLKEASV-----KIL 620			
Db	296	LAAG-----VQETVGVV-----EAHGCTGPICDPIETRSLARV-YG 332	Db	316	ISPAETFQELYDPEFTLVAGYLESOQNTRVASECULVSFLANCVPKEAILEPSLFDDEXV 375			
Qy	504	QGSPILLAANTMARI GAEHVYKASAMQALQKVF-----PSRYTDRNSAEPKDVQETVFS 555	Qy	621	AAGVAI----GHISLFSQKYFKS-----SSSFORDKDMVSSMSEDVATIGSVRADDBE 669			
Db	333	AGTPCALSAKSNGHSTASAGTVGLIKALLSLRHGVPPFLHFLNRPDELSDV----- 386	Db	376	QQLVKVVEGHLTVQYQAAWMETFNVLGAMFDAFRWQANPYLLSV--VKSIGEIRGNDSP 432			
Qy	556	VDPVGNNVGRDGEPCVTAEAVRPSENFETDNYA-IRAGYSESSVDETTVEMSVADMLKE 614	Qy	670	ALPRMDARTAENIVSKWQKIKSLAOFOPDH1EMLP----EVLDGRMRMKIWTDRAAETAQ 725			
Db	387	-----ETGLFLVFOQAVTPWPN----GNDHTPKRVAVSSFGHSIGNTVHAIVEAAPAE 432	Db	433	A----GKQEADEVLGKAIR----ANGPEAVINVLPLNLAKPVKGOPERAW-----ML 476			
Qy	615	ASTKILLAAGVVA-IGLISLFSQYKFLKSSSSFQRKDMVSSMSEDVATIGSVRADDSBALP R 673	Qy	726	GLYYDT-----LLKLSVDSVTSVADGTRVLEASCLSVDLHVPPENNATDVRYTYTR 781			
Db	433	ASAPESSPSDAAVG----PRLEMISSTS-----IEMLPVLDGML 712	Db	477	PLRDYTNTNTLNLAHKFSELVPLSAIMQRVIE-----HQGCEKNIHIFIETV 523			
Qy	674	MDDARTAENIVSKWQK-----IKSLAFCGPDH-----IEMLPVLDGML 712	Qy	782	YEVFWVS 787			
Db	462	QTARQLATWEEHODCVASDLATLARGRRHRPVRTAVVAAANLDELVEGLREVADGDAL 521	Db	524	VQQIWS 529			
Qy	713	-----KWW-TDRAETAQQL-----VYDYLKLKSVDSVTVSADGTRALV 752	RESULT 12					
Db	522	YDAVGHGDRGPWVFSQGGSQVAMGTQIASEPFAATTIAK---EPVIAAESGSFVT 578	T30312	pilin biosynthetic protein - <i>Pseudomonas aeruginosa</i>				
Qy	753	EA-TLEESACSLDVLHPPENATDVRYTRYEVFWSKSG 790	C.Species:	<i>Pseudomonas aeruginosa</i>				
Db	579	EATAQQITVTGIDKQPAVFAVQVALAATMEQTYGVRP G 617	C.Accession:	T30312 #sequence_revision 22-Oct-1999				
Qy	hypothetical protein B1D1.160 [imported] - <i>Neurospora crassa</i>					#text_change 04-Mar-2000		
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Matches	159; Conservative	105; Mismatches	291;	Indels	239;	Gaps	36;
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db	19 ETLKQARQALEAPVNPODPTRMR-----FCLTYY-HQVGTLOMVEFYGAA 64	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
dy	183 --TIVLRLRGEEALLKERPLPKSPKQDVVLVMAFLDVSNDAMALDPDF-----ITGYE 234	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
db	65 LLABEMEQLVQALLDGRVPNQGEALEVLMAQILQLPVYLDRIQTAERDLPVVPLNDL 124	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
dy	235 FVEEALKLQOEGGASSLAPDL--RAQID-----ETLEBITPRTVYLELLGLP 278	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
db	125 RAARGEKLISE--TSLFAPDLSQRPQDGEAIAQLRTDELGGGLRKLRQTOQMALVYGLL 182	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
dy	279 LGDDYAAK-----RNGLSSGTYN--LWSVGCGGASALVGQHTRKEPMNEAFLRMT 327	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
db	183 RNDQVATSGYLGLARYARLEGGLCRAAPLGPIWSI---ASGLVEGLANGSVNSASVY-T 237	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
dy	328 AAEQVD-----LFWATPSNI-----PAESPEVYEVALVAQAFIG 363	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
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dy	364 KKPHLQDA--DROFQQLQKQKNAMEIPAM-----LYDTRNNWEFLDFGLBERG-- 409	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
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db	347 SELDALLAPLKLQIAIDLTLAVLGFGQPRKVILDQDLYTHALAQGRREPSDALIMDVAGALLY 406	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
dy	462 LETWLAGVYFP-RFRDTKQKKFKLQGDYYD-----DPMVLSYL----- 497	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	
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RESULT 15
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C;Species
C;Date: 0
C;Accession
R;Uchiyama
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A;Descrip
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